

OM protein - protein search, using sw model
Run on: October 21, 2006, 18:10:31 ; Search time 198 Seconds
(without alignments)
794.356 Million cell updates/sec

Title: US-09-981-915a-523
Perfect score: 1806
Sequence: 1 MKTIQPKVHNSISWAIFTGL.....RRAGCVMLPLVLVHLLKF 344
Scoring table: BLOSUM62
Gapop 10.0 ; Gapext 0.5
Searched: 2589679 seqs, 457216429 residues
Total number of hits satisfying chosen parameters: 2589679
Minimum DB seq length: 0
Minimum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries
Database : A_Geneseq_8:*

- 1: Geneseqp1980s:*
- 2: Geneseqp1990s:*
- 3: Geneseqp2000s:*
- 4: Geneseqp2001s:*
- 5: Geneseqp2002s:*
- 6: Geneseqp2003as:*
- 7: Geneseqp2003bs:*
- 8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

No.	Score	Match Length	DB ID	Description
RESULT 1				
ID	AA57601	standard; protein; 344 AA.		
DE	Human protein SEQ ID NO:1.			
PN	WO958668-A1.			
PD	18-NOV-1999.			
PA	(ONON) ONO PHARM CO LTD.			
Query Match	100.0%;	Score 1806; DB 3; Length 344;		
Best Local Similarity	100.0%;	Pred. No. 5.3e-147;		
RESULT 2				
ID	AA844329	standard; protein; 344 AA.		
DE	Human PRO337 protein sequence SEQ ID NO:523.			
PN	WO200053756-A2.			
PD	14-SEP-2000.			
PA	(GETH) GENENTECH INC.			
Query Match	100.0%;	Score 1806; DB 3; Length 344;		
Best Local Similarity	100.0%;	Pred. No. 5.3e-147;		
RESULT 3				
ID	AA831204	standard; protein; 344 AA.		
DE	Amino acid sequence of human polypeptide PRO337.			
PN	WO200077037-A2.			
PD	21-DEC-2000.			
PA	(GETH) GENENTECH INC.			
Query Match	100.0%;	Score 1806; DB 4; Length 344;		
Best Local Similarity	100.0%;	Pred. No. 5.3e-147;		
RESULT 4				
ID	AAU12359	standard; protein; 344 AA.		
DE	Human PRO337 polypeptide sequence.			
PN	WO200140466-A2.			
PD	07-JUN-2001.			
PA	(GETH) GENENTECH INC.			
Query Match	100.0%;	Score 1806; DB 4; Length 344;		
Best Local Similarity	100.0%;	Pred. No. 5.3e-147;		
RESULT 5				
ID	AAU83654	standard; protein; 344 AA.		
DE	Human PRO protein, Seq ID No 126.			
PN	WO200208288-A2.			
PD	31-JAN-2002.			
PA	(GETH) GENENTECH INC.			
Query Match	100.0%;	Score 1806; DB 5; Length 344;		
Best Local Similarity	100.0%;	Pred. No. 5.3e-147;		
RESULT 6				
ID	ABR84844	standard; protein; 344 AA.		
DE	Human PRO337 protein sequence SEQ ID NO:56.			

PN	WO200200690-A2.			
PD	03-JAN-2002.			
PA	(GETH) GENENTECH INC.			
Query Match	100.0%;	Score 1806; DB 5; Length 344;		
Best Local Similarity	100.0%;	Pred. No. 5.3e-147;		
RESULT 7				
ID	AB95450	standard; protein; 344 AA.		
DE	Human angio genesis related protein PRO337 SEQ ID NO: 56.			
PN	WO200208284-A2.			
PD	31-JAN-2002.			
PA	(GETH) GENENTECH INC.			
PA	(BAKE)/ BAKER K P.			
PA	(FERR)/ FERRARA N.			
PA	(GERB)/ GERBER H.			
PA	(GERR)/ GERRITSEN M E.			
PA	(GODD)/ GODDARD A.			
PA	(GODO)/ GODOWSKI P J.			
PA	(GURN)/ GURNEY A L.			
PA	(HILL)/ HILLAN K J.			
PA	(MARS)/ MARSTERS S A.			
PA	(PANJ)/ PAN J.			
PA	(PAON)/ PAONI N F.			
PA	(STEP)/ STEPHAN J F.			
PA	(WATA)/ WATANABE C K.			
PA	(WILL)/ WILLIAMS P M.			
PA	(WOOD)/ WOOD W I.			
Query Match	100.0%;	Score 1806; DB 5; Length 344;		
Best Local Similarity	100.0%;	Pred. No. 5.3e-147;		
RESULT 8				
ID	ADY31866	standard; protein; 344 AA.		
DE	Novel human secreted and transmembrane protein PRO337.			
PN	WO200193983-A1.			
PD	13-DEC-2001.			
PA	(GETH) GENENTECH INC.			
Query Match	100.0%;	Score 1806; DB 5; Length 344;		
Best Local Similarity	100.0%;	Pred. No. 5.3e-147;		
RESULT 9				
ID	ABO17803	standard; protein; 344 AA.		
DE	Novel human secreted and transmembrane protein PRO337.			
PN	US2003032156-A1.			
PD	13-FEB-2003.			
PA	(GETH) GENENTECH INC.			
Query Match	100.0%;	Score 1806; DB 6; Length 344;		
Best Local Similarity	100.0%;	Pred. No. 5.3e-147;		
RESULT 10				
ID	ABU80801	standard; protein; 344 AA.		
DE	Human PRO polypeptide #63.			
PN	US2003036635-A1.			
PD	20-FEB-2003.			
PA	(GETH) GENENTECH INC.			
Query Match	100.0%;	Score 1806; DB 6; Length 344;		
Best Local Similarity	100.0%;	Pred. No. 5.3e-147;		
RESULT 11				
ID	ABO25175	standard; protein; 344 AA.		
DE	Novel human secreted and transmembrane protein PRO337.			
PN	US2003040014-A1.			
PD	27-FEB-2003.			
PA	(GETH) GENENTECH INC.			
Query Match	100.0%;	Score 1806; DB 6; Length 344;		
Best Local Similarity	100.0%;	Pred. No. 5.3e-147;		
RESULT 12				
ID	ABO25275	standard; protein; 344 AA.		
DE	Novel human secreted and transmembrane protein PRO337.			
PN	US2003050239-A1.			
PD	13-MAR-2003.			
PA	(GETH) GENENTECH INC.			
Query Match	100.0%;	Score 1806; DB 6; Length 344;		
Best Local Similarity	100.0%;	Pred. No. 5.3e-147;		
RESULT 13				
ID	ABO33767	standard; protein; 344 AA.		
DE	Novel human secreted and transmembrane protein PRO337.			
PN	US2003045687-A1.			
PD	06-MAR-2003.			

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PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 14
ID ABU81057 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US200304311-A1.
PD 02-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 15
ID ABU7281 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2002192706-A1.
PD 19-DEC-2002.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 16
ID ABU6757 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003036180-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 17
ID ABU67293 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003032063-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 18
ID ABU84961 standard; protein; 344 AA.
DE Human secreted and transmembrane PRO polypeptide #37.
PN US2002177553-A1.
PD 28-NOV-2002.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 19
ID ABU5938 standard; protein; 344 AA.
DE Novel secreted and transmembrane protein PRO337.
PN US2003017563-A1.
PD 23-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 20
ID ABU61159 standard; protein; 344 AA.
DE Human PRO337 polypeptide.
PN US2002169284-A1.
PD 14-NOV-2002.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 21
ID AB025028 standard; protein; 344 AA.
DE Human secreted/transmembrane protein (PRO) #188.
PN US2003036179-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 22
ID ABU72061 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2002177165-A1.
PD 28-NOV-2002.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 23
ID ABU67162 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003032062-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 24
ID ABU80428 standard; protein; 344 AA.
DE Human secreted/transmembrane protein PRO337.
PN US2003004102-A1.
PD 02-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 25
ID ABU82110 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003088063-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 26
ID ABU67033 standard; protein; 344 AA.
DE Human secreted/transmembrane, PRO, protein SEQ ID 376.
PN US2003032155-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 27
ID ABU79804 standard; protein; 344 AA.
DE Human secreted/transmembrane protein PRO337.
PN US2003032057-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 28
ID ADA45895 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003022328-A1.
PD 30-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 29
ID ADA76326 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003073212-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 30
ID ABJ72290 standard; protein; 344 AA.
DE Human PRO337 protein.
PN US2003050448-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 31
ID ADA18976 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003054517-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
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Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 32
ID ADA61599 standard; protein; 344 AA.
DE Homo sapiens.
PN US2003049816-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 33
ID ADB19384 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003068796-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 34
ID ADB27925 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003082704-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 35
ID ADA86404 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003082711-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 36
ID ADB15968 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003087350-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 37
ID ADA47754 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003073215-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 38
ID ADA67549 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003068795-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 39
ID ADB30556 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003068794-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 40
ID ADA85852 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003082693-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 41
ID ADA97064 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003082705-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 42
ID ADA79368 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003082763-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 43
ID ADA87507 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003087345-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 44
ID ADB16709 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003087349-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 45
ID ADA91801 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003082694-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 46
ID ADB14864 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003087351-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 47
ID ADA25062 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003050241-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 48
ID ADA47276 standard; protein; 344 AA.
DE Human secreted/transmembrane polypeptide PRO337.
PN US2003044844-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 49
ID ADB18825 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003073211-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 50

ID ADA94040 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003077722-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 51
ID ADB19936 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003082691-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 52
ID ADB13248 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003082710-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 53
ID ABO43336 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003044945-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 54
ID ABO19730 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003050240-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 55
ID ADA12723 standard; protein; 344 AA.
DE Human secreted/transmembrane polypeptide PRO337.
PN US2003055216-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 56
ID ADA74502 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003068798-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 57
ID ADB24735 standard; protein; 344 AA.
DE Human PRO polypeptide SEQ ID NO 376.
PN US2003077713-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 58
ID ADA82259 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003082701-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 59
ID ADA75222 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003077721-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 60
ID ADA85300 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003082695-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 61
ID ADA84748 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003082708-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 62
ID ADB30004 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003073214-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 63
ID ADA80532 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003082761-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 64
ID ADA75774 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003082703-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 65
ID ADA46999 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003073210-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 66
ID ADB25295 standard; protein; 344 AA.
DE Human PRO polypeptide SEQ ID NO 376.
PN US2003077715-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 67
ID ADA93471 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003077721-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 68
ID ADB26821 standard; protein; 344 AA.
DE Human PRO polypeptide #188.

PN US2003092147-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 69
ID ADB31108 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003096386-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 70
ID ABJ72418 standard; protein; 344 AA.
DE Human PRO337 protein.
PN US2003027988-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 71
ID ADA61036 standard; protein; 344 AA.
DE Homo sapiens.
PN US2003049817-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 72
ID ADB24183 standard; protein; 344 AA.
DE Human PRO polypeptide SEQ ID NO 376.
PN US2003077714-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 73
ID ADA96512 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003082690-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 74
ID ADA81084 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003082702-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 75
ID ADA95960 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003082759-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 76
ID ADB26269 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003082760-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 77
ID ADB21754 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003082765-A1.

PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 78
ID ABO34313 standard; protein; 344 AA.
DE Human secreted/transmembrane polypeptide PRO 337.
PN US2003044934-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 79
ID ABO19621 standard; protein; 344 AA.
DE Novel human secreted and transmembrane polypeptide #89.
PN US2003049633-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 80
ID ADA77533 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003068797-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 81
ID ADB18273 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003077710-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 82
ID ADA86956 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003082709-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 83
ID ADA88059 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003082700-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 84
ID ADA46447 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003054516-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 85
ID ADB28477 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003082699-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 86
ID ADB29029 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003082706-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.

Query Match	100.0%;	Score 1806;	DB 7;	Length 344;
Best Local Similarity	100.0%;	Pred. No. 5.3e-147;		
RESULT 87				
ID ADA76981 standard; protein; 344 AA.				
DE Human PRO polypeptide #188.				
PN US2003059909-A1.				
PD 27-MAR-2003.				
PA (GETH) GENENTECH INC.				
Query Match	100.0%;	Score 1806;	DB 7;	Length 344;
Best Local Similarity	100.0%;	Pred. No. 5.3e-147;		
RESULT 88				
ID ADA8611 standard; protein; 344 AA.				
DE Novel human secreted and transmembrane protein PRO337.				
PN US2003073213-A1.				
PD 17-APR-2003.				
PA (GETH) GENENTECH INC.				
Query Match	100.0%;	Score 1806;	DB 7;	Length 344;
Best Local Similarity	100.0%;	Pred. No. 5.3e-147;		
RESULT 89				
ID ADA97616 standard; protein; 344 AA.				
DE Human PRO polypeptide #188.				
PN US2003082686-A1.				
PD 01-MAY-2003.				
PA (GETH) GENENTECH INC.				
Query Match	100.0%;	Score 1806;	DB 7;	Length 344;
Best Local Similarity	100.0%;	Pred. No. 5.3e-147;		
RESULT 90				
ID ADB27373 standard; protein; 344 AA.				
DE Human PRO polypeptide #188.				
PN US2003022239-A1.				
PD 30-JAN-2003.				
PA (GETH) GENENTECH INC.				
Query Match	100.0%;	Score 1806;	DB 7;	Length 344;
Best Local Similarity	100.0%;	Pred. No. 5.3e-147;		
RESULT 91				
ID ADB22306 standard; protein; 344 AA.				
DE Novel human secreted and transmembrane protein PRO337.				
PN US2003087344-A1.				
PD 08-MAY-2003.				
PA (GETH) GENENTECH INC.				
Query Match	100.0%;	Score 1806;	DB 7;	Length 344;
Best Local Similarity	100.0%;	Pred. No. 5.3e-147;		
RESULT 92				
ID ABO19862 standard; protein; 344 AA.				
DE Human secreted/transmembrane protein PRO337.				
PN US2003044902-A1.				
PD 06-MAR-2003.				
PA (GETH) GENENTECH INC.				
Query Match	100.0%;	Score 1806;	DB 7;	Length 344;
Best Local Similarity	100.0%;	Pred. No. 5.3e-147;		
RESULT 93				
ID ABJ72120 standard; protein; 344 AA.				
DE Human membrane bound receptor/protein PRO337 amino acid sequence.				
PN US2003065147-A1.				
PD 03-APR-2003.				
PA (GETH) GENENTECH INC.				
Query Match	100.0%;	Score 1806;	DB 7;	Length 344;
Best Local Similarity	100.0%;	Pred. No. 5.3e-147;		
RESULT 94				
ID ADA66997 standard; protein; 344 AA.				
DE Human PRO polypeptide #188.				
PN US2003068793-A1.				
PD 10-APR-2003.				
PA (GETH) GENENTECH INC.				
Query Match	100.0%;	Score 1806;	DB 7;	Length 344;
Best Local Similarity	100.0%;	Pred. No. 5.3e-147;		
RESULT 95				
ID ADB22858 standard; protein; 344 AA.				
DE Human PRO polypeptide #188.				
PN US2003077711-A1.				
PD 24-APR-2003.				
PA (GETH) GENENTECH INC.				
Query Match	100.0%;	Score 1806;	DB 7;	Length 344;
Best Local Similarity	100.0%;	Pred. No. 5.3e-147;		
RESULT 96				
ID ADB66588 standard; protein; 344 AA.				
DE Novel human secreted and transmembrane protein PRO337.				
PN US2003087347-A1.				
PD 08-MAY-2003.				
PA (GETH) GENENTECH INC.				
Query Match	100.0%;	Score 1806;	DB 7;	Length 344;
Best Local Similarity	100.0%;	Pred. No. 5.3e-147;		
RESULT 97				
ID ADA92353 standard; protein; 344 AA.				
DE Novel human secreted and transmembrane protein PRO337.				
PN US2003082712-A1.				
PD 01-MAY-2003.				
PA (GETH) GENENTECH INC.				
Query Match	100.0%;	Score 1806;	DB 7;	Length 344;
Best Local Similarity	100.0%;	Pred. No. 5.3e-147;		
RESULT 98				
ID ADB15416 standard; protein; 344 AA.				
DE Human PRO polypeptide #188.				
PN US2003087352-A1.				
PD 08-MAY-2003.				
PA (GETH) GENENTECH INC.				
Query Match	100.0%;	Score 1806;	DB 7;	Length 344;
Best Local Similarity	100.0%;	Pred. No. 5.3e-147;		

DE Novel human secreted and transmembrane protein PRO337.
PN US2003082689-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 106
ID ADB84993 standard; protein; 344 AA.
DE Human PRO polypeptide #63.
PN US2003073817-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 107
ID ADB89668 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003082698-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 108
ID ADB90400 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003082762-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 109
ID ADB39501 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003082764-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 110
ID ADB78099 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003092886-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 111
ID ADB74029 standard; protein; 344 AA.
DE Human PRO polypeptide #89.
PN US2003045462-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 112
ID ADB87165 standard; protein; 344 AA.
DE Human PRO polypeptide #63.
PN US2003088067-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 113
ID ADB84747 standard; protein; 344 AA.
DE Human PRO polypeptide #63.
PN US2003092890-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 114
ID ADB47124 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.

PN US2003082687-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 115
ID ADB83862 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003069397-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 116
ID ADB86731 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003082697-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 117
ID ADB73017 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003092887-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 118
ID ADB76745 standard; protein; 344 AA.
DE Human PRO polypeptide #89.
PN US2003083248-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 119
ID ADB77336 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003082696-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 120
ID ADB34493 standard; protein; 344 AA.
DE Human PRO polypeptide SEQ ID NO 376.
PN US2003077717-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 121
ID ADB35597 standard; protein; 344 AA.
DE Human PRO polypeptide SEQ ID NO 376.
PN US2003077719-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 122
ID ADB33941 standard; protein; 344 AA.
DE Human PRO polypeptide SEQ ID NO 376.
PN US2003077716-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 123
ID ADB35045 standard; protein; 344 AA.
DE Human PRO polypeptide SEQ ID NO 376.
PN US2003077718-A1.

PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 124
ID ADB36149 standard; protein; 344 AA.
DE Human PRO polypeptide SEQ ID NO 376.
PN US2003077720-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 125
ID ADB46544 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003082692-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 126
ID ADC44171 standard; protein; 344 AA.
DE Human secreted/transmembrane protein, PRO337.
PN US2003054986-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 127
ID ADC61931 standard; protein; 344 AA.
DE Human secreted/transmembrane protein, PRO337.
PN US2003049684-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 128
ID ADC63895 standard; protein; 344 AA.
DE Human secreted/transmembrane protein, PRO337.
PN US2003054405-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 129
ID ADC66995 standard; protein; 344 AA.
DE Human secreted/transmembrane protein, PRO337.
PN US2003060406-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 130
ID ADC69119 standard; protein; 344 AA.
DE Human secreted/transmembrane protein, PRO337.
PN US2003064407-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 131
ID ADC63179 standard; protein; 344 AA.
DE Human secreted/transmembrane protein, PRO337.
PN US2003068648-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 132
ID ADC68244 standard; protein; 344 AA.
DE Human secreted/transmembrane protein, PRO337.
PN US2003069178-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 133
ID ADC41564 standard; protein; 344 AA.
DE Human secreted/transmembrane protein, PRO337.
PN US2003072745-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 134
ID ADC67619 standard; protein; 344 AA.
DE Human secreted/transmembrane protein, PRO337.
PN US2003073131-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 135
ID ADC62555 standard; protein; 344 AA.
DE Human secreted/transmembrane protein, PRO337.
PN US2003073624-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 136
ID ADC36855 standard; protein; 344 AA.
DE Human PRO polypeptide #63.
PN US2003088055-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 137
ID ADC42188 standard; protein; 344 AA.
DE Human secreted/transmembrane protein, PRO337.
PN US2003104998-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 138
ID ADC21845 standard; protein; 344 AA.
DE Human PRO polypeptide #63.
PN US2003096969-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 139
ID ADC50417 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003092106-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 140
ID ADC71964 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003092107-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 141
ID ADC59943 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003092105-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.

Query Match
Best Local Similarity 100.0%; Score 1806; DB 7; Length 344;
RESULT 142
ID ADC49876 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003088064-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1806; DB 7; Length 344;
RESULT 143
ID ADC49075 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003088070-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1806; DB 7; Length 344;
RESULT 144
ID ADC49592 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003088071-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1806; DB 7; Length 344;
RESULT 145
ID ADC47453 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003088072-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1806; DB 7; Length 344;
RESULT 146
ID ADC52950 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein Seq ID376.
PN US2003087365-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1806; DB 7; Length 344;
RESULT 147
ID ADC57304 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein Seq ID376.
PN US2003087366-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1806; DB 7; Length 344;
RESULT 148
ID ADC60495 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003087367-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1806; DB 7; Length 344;
RESULT 149
ID ADC50970 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003087361-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1806; DB 7; Length 344;
RESULT 150
ID ADC65497 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003087362-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1806; DB 7; Length 344;

Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 151
ID ADC54595 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein Seq ID376.
PN US2003087363-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1806; DB 7; Length 344;
RESULT 152
ID ADC53556 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein Seq ID376.
PN US2003087364-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1806; DB 7; Length 344;
RESULT 153
ID ADC59079 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein Seq ID376.
PN US2003087359-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1806; DB 7; Length 344;
RESULT 154
ID ADC55957 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein Seq ID376.
PN US2003087360-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1806; DB 7; Length 344;
RESULT 155
ID ADC58527 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein Seq ID376.
PN US2003087346-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1806; DB 7; Length 344;
RESULT 156
ID ADC47198 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003105288-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1806; DB 7; Length 344;
RESULT 157
ID ADD03201 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003092104-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1806; DB 7; Length 344;
RESULT 158
ID ADC90193 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003087348-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1806; DB 7; Length 344;
RESULT 159
ID ADC69612 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003194770-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1806; DB 7; Length 344;
RESULT 160
ID ADC65497 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003087362-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1806; DB 7; Length 344;

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RESULT 160
ID ADC48501 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003194773-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 161
ID ADD10030 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003194776-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 162
ID ADC78073 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003096972-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 163
ID ADD04605 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003087354-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 164
ID ADD06308 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003073816-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 165
ID ADC80561 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003092103-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 166
ID ADD11068 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003194774-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 167
ID ADD10345 standard; protein; 344 AA.
DE Human secreted/transmembrane PRO polypeptide #28.
PN US2003105011-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 168
ID ADC47949 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003194771-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 169
ID ADC77827 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003088066-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 170
ID ADC80009 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003087358-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 171
ID ADD11305 standard; protein; 344 AA.
DE Human secreted/transmembrane PRO polypeptide #28.
PN US2003105013-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 172
ID ADD03478 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003194775-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 173
ID ADD50790 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003105291-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 174
ID ADD41191 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003203438-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 175
ID ADD52330 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003194769-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 176
ID ADD51036 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003105290-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 177
ID ADD53070 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003194792-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 178
ID ADD53622 standard; protein; 344 AA.
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DE Novel human secreted and transmembrane protein PRO337.
PD US2003203437-A1.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 179
ID ADD37098 standard; protein; 344 AA.
DE Human secreted/transmembrane PRO polypeptide #28.
PN US2003105012-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 180
ID ADD51778 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003194779-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 181
ID ADD02577 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003203431-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 182
ID ADD0517 standard; protein; 344 AA.
DE Human PRO polypeptide #63.
PN US2003096971-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 183
ID ADD02011 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003203430-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 184
ID ADD54193 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003203432-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 185
ID ADD50271 standard; protein; 344 AA.
DE Human PRO polypeptide #63.
PN US2003096970-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 186
ID ADD51282 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003105289-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 187
ID ADE49557 standard; protein; 344 AA.
DE Human secreted/transmembrane protein, PRO337.

PN US2003096744-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 188
ID ADD92510 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003199030-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 189
ID ADD91406 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003199055-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 190
ID ADE04020 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003199057-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 191
ID ADE32317 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003194765-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 192
ID ADE22249 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003199056-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 193
ID ADD79473 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003203428-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 194
ID ADE35611 standard; protein; 344 AA.
DE Human secreted/transmembrane protein, PRO337.
PN US2003203434-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 195
ID ADE16725 standard; protein; 344 AA.
DE Human secreted/transmembrane protein, PRO337.
PN US2003203435-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 196
ID ADD73340 standard; protein; 344 AA.
DE Human secreted/transmembrane protein, PRO337.
PN US2003203436-A1.

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PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 1806; DB 7; Length 344;
  Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 197
  ID ADE42009 standard; protein; 344 AA.
  DE Human PRO polypeptide #188.
  PN US2003194772-A1.
  PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 1806; DB 7; Length 344;
  Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 198
  ID ADE17826 standard; protein; 344 AA.
  DE Human PRO polypeptide #188.
  PN US2003199023-A1.
  PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 1806; DB 7; Length 344;
  Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 199
  ID ADD91958 standard; protein; 344 AA.
  DE Human PRO polypeptide #188.
  PN US2003199053-A1.
  PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 1806; DB 7; Length 344;
  Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 200
  ID ADE33421 standard; protein; 344 AA.
  DE Novel human secreted and transmembrane protein PRO337.
  PN US2003194767-A1.
  PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 1806; DB 7; Length 344;
  Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 201
  ID ADE33973 standard; protein; 344 AA.
  DE Novel human secreted and transmembrane protein PRO337.
  PN US2003194791-A1.
  PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 1806; DB 7; Length 344;
  Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 202
  ID ADD80025 standard; protein; 344 AA.
  DE Human PRO polypeptide #188.
  PN US2003207417-A1.
  PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 1806; DB 7; Length 344;
  Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 203
  ID AD93062 standard; protein; 344 AA.
  DE Human PRO polypeptide #188.
  PN US2003194768-A1.
  PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 1806; DB 7; Length 344;
  Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 204
  ID ADD72698 standard; protein; 344 AA.
  DE Human secreted/transmembrane protein, PRO337.
  PN US2003194781-A1.
  PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 1806; DB 7; Length 344;
  Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 205
  ID ADE19482 standard; protein; 344 AA.
  DE Human PRO polypeptide #188.
  PN US2003199025-A1.
  PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 1806; DB 7; Length 344;
  Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 206
  ID ADE18930 standard; protein; 344 AA.
  DE Human PRO polypeptide #188.
  PN US2003199026-A1.
  PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 1806; DB 7; Length 344;
  Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 207
  ID ADE43126 standard; protein; 344 AA.
  DE Human PRO polypeptide #188.
  PN US2003199033-A1.
  PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 1806; DB 7; Length 344;
  Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 208
  ID ADD95915 standard; protein; 344 AA.
  DE Human PRO polypeptide #188.
  PN US2003199059-A1.
  PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 1806; DB 7; Length 344;
  Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 209
  ID ADE22801 standard; protein; 344 AA.
  DE Human PRO polypeptide #188.
  PN US2003199064-A1.
  PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 1806; DB 7; Length 344;
  Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 210
  ID ADD78919 standard; protein; 344 AA.
  DE Human PRO polypeptide #188.
  PN US2003203429-A1.
  PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 1806; DB 7; Length 344;
  Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 211
  ID ADE32869 standard; protein; 344 AA.
  DE Novel human secreted and transmembrane protein PRO337.
  PN US2003194766-A1.
  PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 1806; DB 7; Length 344;
  Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 212
  ID ADE42561 standard; protein; 344 AA.
  DE Human PRO polypeptide #188.
  PN US2003199032-A1.
  PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 1806; DB 7; Length 344;
  Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 213
  ID ADE17349 standard; protein; 344 AA.
  DE Human secreted/transmembrane protein, PRO337.
  PN US2003203433-A1.
  PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 1806; DB 7; Length 344;
  Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 214
  ID ADD80577 standard; protein; 344 AA.
  DE Human PRO polypeptide #188.
  PN US2003207418-A1.
  PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
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Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 224
ID ADG53120 standard; protein; 344 AA.
DE Human secreted/transmembrane protein, PRO3337.
FN US2003216561-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 225
ID ADG60440 standard; protein; 344 AA.
DE Human secreted/transmembrane protein, PRO3337.
FN US2003206915-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 226
ID ADG80014 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
FN US2003207372-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 227
ID ADG63785 standard; protein; 344 AA.
DE Human secreted/transmembrane polypeptide PRO3337.
FN US2003170721-A1.
PD 11-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 228
ID ADH5306 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO3337.
FN US2003207381-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 229
ID ADH5858 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO3337.
FN US2003207379-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 230
ID ADI61200 standard; protein; 344 AA.
DE Human secreted/transmembrane protein, PRO3337.
FN US2003077700-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 231
ID ADI64077 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO3337.
FN US2003207385-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 232
ID ADI65026 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO3337.
FN US2003207386-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;

RESULT 233
ID ADL63525 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003207387-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 234
ID ADH81939 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003207388-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 235
ID ADH81387 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003207377-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 236
ID ADH82556 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003087355-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 237
ID ADN15955 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003087353-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 238
ID ADN16584 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003087385-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 239
ID ADN15403 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003087356-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 240
ID ADN14851 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003087357-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 241
ID ADC48829 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003092888-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 242
ID ADC39051 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003100717-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 243
ID ADE21000 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003100735-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 244
ID ADE05844 standard; protein; 344 AA.
DE Human PRO polypeptide #63.
PN US2003100728-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 245
ID ADD76561 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003100087-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 246
ID ADD75073 standard; protein; 344 AA.
DE Human PRO polypeptide #63.
PN US2003100712-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 247
ID ADD75819 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003100717-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 248
ID ADD85051 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003100722-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 249
ID ADD86877 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003100738-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 250
ID ADE20754 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003100734-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 251
ID ADE39051 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003100734-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 252
ID ADE39051 standard; protein; 344 AA.

DE Novel human secreted and transmembrane protein PRO337.
PN US2003096362-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 252
ID AD87925 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003092113-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 253
ID AD86329 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003203440-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 254
ID AD80598 standard; protein; 344 AA.
DE Human PRO polypeptide #63.
PN US2003100727-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 255
ID AD73583 standard; protein; 344 AA.
DE Human PRO polypeptide #63.
PN US2003100711-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 256
ID ADE75777 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003211571-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 257
ID ADE4857 standard; protein; 344 AA.
DE Human secreted/transmembrane protein, PRO337.
PN US2003104536-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 258
ID AD78423 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003100737-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 259
ID AD841306 standard; protein; 344 AA.
DE Human secreted/transmembrane PRO polypeptide #28.
PN US2003100497-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 260
ID AD823353 standard; protein; 344 AA.
DE Human PRO polypeptide #188.

PN US2003092108-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 261
ID ADE21246 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003100736-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 262
ID ADD7361 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003100732-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 263
ID ADE20508 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003100733-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 264
ID ADD75573 standard; protein; 344 AA.
DE Human PRO polypeptide #63.
PN US2003100064-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 265
ID ADD74089 standard; protein; 344 AA.
DE Human PRO polypeptide #63.
PN US2003100708-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 266
ID ADD74335 standard; protein; 344 AA.
DE Human PRO polypeptide #63.
PN US2003100709-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 267
ID ADD76065 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003100718-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 268
ID AD85557 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003100721-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 269
ID ADE23905 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003092110-A1.

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PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 270
ID ADE24548 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003092111-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 271
ID ADD87373 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003203439-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 272
ID ADE05106 standard; protein; 344 AA.
DE Human PRO polypeptide #63.
PN US2003100726-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 273
ID ADD75319 standard; protein; 344 AA.
DE Human PRO polypeptide #63.
PN US2003100714-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 274
ID ADD76863 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003100715-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 275
ID ADD86631 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003100719-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 276
ID ADE89239 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003199062-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 277
ID ADE41199 standard; protein; 344 AA.
DE Human secreted/transmembrane polypeptide PRO337.
PN US2003104558-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 278
ID ADD78099 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003100731-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 279
ID ADE18378 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003194794-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 280
ID ADE89687 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003199054-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 281
ID ADE89958 standard; protein; 344 AA.
DE Human secreted/transmembrane protein, PRO337.
PN US2003130181-A1.
PD 10-JUL-2003.
PA (ASHK/) ASHKENAZI A J.
PA (BAKE/) BAKER K P.
PA (BOTS/) BOTSTEIN D.
PA (DESN/) DESNOYERS L.
PA (EATO/) EATON D L.
PA (FERR/) FERRARA N.
PA (FILV/) FILVAROFF E.
PA (FONG/) FONG S.
PA (GAOW/) GAO W.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GIRM/) GIRMALDI J C.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (KLJA/) KLJAVIN I J.
PA (KUOS/) KUO S S.
PA (NAPI/) NAPIER M A.
PA (PANI/) PAN J.
PA (PAON/) PAONI N F.
PA (ROYM/) ROY M A.
PA (SHEL/) SHELTON D L.
PA (STEW/) STEWART T A.
PA (TUMA/) TUNAS D.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 282
ID ADD77607 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003100729-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 283
ID ADD77853 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003100730-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 284
ID ADD85311 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003100725-A1.
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PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 285
ID ADD73843 standard; protein; 344 AA.
DE Human PRO polypeptide #63.
PN US2003100710-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 286
ID ADD74581 standard; protein; 344 AA.
DE Human PRO polypeptide #63.
PN US2003100713-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 287
ID ADD77109 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003100716-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 288
ID ADD85803 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003100720-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 289
ID ADE05352 standard; protein; 344 AA.
DE Human PRO polypeptide #63.
PN US2003100723-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 290
ID ADD74827 standard; protein; 344 AA.
DE Human PRO polypeptide #63.
PN US2003100724-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 291
ID ADF61598 standard; protein; 344 AA.
DE Human secreted/transmembrane protein, PRO337.
PN US2003195345-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 292
ID ADF40290 standard; protein; 344 AA.
DE Human secreted/transmembrane protein, PRO337.
PN US2003198994-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 293
ID ADF46086 standard; protein; 344 AA.
DE Human secreted/transmembrane protein, PRO337.
PN US2003195148-A1.
PD 16-OCT-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 294
ID ADE94707 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US200319027-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 295
ID ADE91118 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003199061-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 296
ID ADE95259 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003199052-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 297
ID ADE93369 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003199060-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 298
ID ADF24482 standard; protein; 344 AA.
DE Human secreted/transmembrane protein, PRO337.
PN US2003204055-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 299
ID ADF40914 standard; protein; 344 AA.
DE Human secreted/transmembrane protein, PRO337.
PN US2003199021-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 300
ID ADF23858 standard; protein; 344 AA.
DE Human secreted/transmembrane protein, PRO337.
PN US2003203402-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 301
ID ADF33841 standard; protein; 344 AA.
DE Human secreted/transmembrane protein, PRO337.
PN US2003194780-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 302
ID ADF34950 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003199029-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.

RESULT 321
ID ADF98625 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003208055-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 322
ID ADG03456 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003207351-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 323
ID ADF99177 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003207353-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 324
ID ADG16762 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003207359-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 325
ID ADG05221 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003207375-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 326
ID ADG19488 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003207425-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 327
ID ADG11256 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003096967-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 328
ID ADG13325 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003207357-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 329
ID ADG08382 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003207424-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 330
ID ADG07758 standard; protein; 344 AA.

ID ADG15552 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003219885-A1.
PD 27-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 331
ID ADG12015 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003096963-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 332
ID ADF96950 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003207371-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 333
ID ADG06135 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003207374-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 334
ID ADG23719 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003207389-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 335
ID ADG04008 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003207423-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 336
ID ADG24909 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003207427-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 337
ID ADF94592 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003096964-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 338
ID ADG07206 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003207350-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 339
ID ADG07758 standard; protein; 344 AA.

DE Novel human secreted and transmembrane protein PRO337.
PN US2003207356-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 340
ID ADG06688 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003096966-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 341
ID ADG52523 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003194778-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 342
ID ADG60917 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003207390-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 343
ID ADG62021 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003207428-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 344
ID ADG82222 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003207358-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 345
ID ADG57461 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003207362-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 346
ID ADG56909 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003207364-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 347
ID ADG55805 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003207365-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 348
ID ADG58565 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.

PN US2003207368-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 349
ID ADG70931 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003207420-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 350
ID ADH39032 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003096965-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 351
ID ADG58013 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003207363-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 352
ID ADG53597 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003207415-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 353
ID ADG71493 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003207421-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 354
ID ADG50696 standard; protein; 344 AA.
DE Human secreted/transmembrane protein, PRO337.
PN US2003207803-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 355
ID ADG81670 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003207805-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 356
ID ADH30632 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003077723-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 357
ID ADG63634 standard; protein; 344 AA.
DE Human secreted/transmembrane polypeptide PRO337.
PN US2003180796-A1.
PD 25-SEP-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 358
ID ADH1199 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003207419-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 359
ID ADG50072 standard; protein; 344 AA.
DE Human secreted/transmembrane protein, PRO337.
PN US2003215905-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 360
ID ADG51944 standard; protein; 344 AA.
DE Human secreted/transmembrane protein, PRO337.
PN US2003215908-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 361
ID ADG52441 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003207414-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 362
ID ADG54149 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003207416-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 363
ID ADG49448 standard; protein; 344 AA.
DE Human secreted/transmembrane protein, PRO337.
PN US2003216305-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 364
ID ADG81118 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003194793-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 365
ID ADG56357 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003207366-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 366
ID ADH12623 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003207378-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 367
ID ADG48824 standard; protein; 344 AA.
DE Human secreted/transmembrane protein, PRO337.
PN US2003216560-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 368
ID ADG61469 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003207429-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 369
ID ADH28556 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003202331-A1.
PD 30-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 370
ID ADG54701 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003207367-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 371
ID ADG59741 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003207369-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 372
ID ADG51320 standard; protein; 344 AA.
DE Human secreted/transmembrane protein, PRO337.
PN US2004005312-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 373
ID ADH43489 standard; protein; 344 AA.
DE Human PRO polypeptide #28.
PN US2003224984-A1.
PD 04-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 374
ID ADG59264 standard; protein; 344 AA.
DE Human secreted/transmembrane protein, PRO337.
PN US2004005657-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 375
ID ADG34122 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2004006206-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;

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Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 376
ID ADG62720 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2004006219-A1.
PD 08-JAN-2004.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 377
ID ADI18165 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003207361-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 378
ID ADI33592 standard; protein; 344 AA.
DE Human PRO polypeptide #63.
PN US2003096960-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 379
ID ADH69686 standard; protein; 344 AA.
DE Human PRO polypeptide #63.
PN US2004019183-A1.
PD 29-JAN-2004.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 380
ID ADH25745 standard; protein; 344 AA.
DE Human PRO337 protein SEQ ID NO:523.
PN EPI386931-A1.
PD 04-FEB-2004.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 381
ID ADG09908 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2004009548-A1.
PD 15-JAN-2004.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 382
ID ADI15379 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003207382-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 383
ID ADG09256 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2004009547-A1.
PD 15-JAN-2004.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 384
ID ADI14711 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003207383-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 385
ID ADI29847 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003096961-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 386
ID ADI18306 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003207349-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 387
ID ADM27244 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2004044179-A1.
PD 04-MAR-2004.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 388
ID ADJ63587 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2004039164-A1.
PD 26-FEB-2004.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 389
ID ADJ77482 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2004038336-A1.
PD 26-FEB-2004.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 390
ID ADK82834 standard; protein; 344 AA.
DE Human PRO polypeptide #28.
PN US2004043927-A1.
PD 04-MAR-2004.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 391
ID ADK66602 standard; protein; 344 AA.
DE Human PRO polypeptide #63.
PN US2004044180-A1.
PD 04-MAR-2004.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 392
ID ADJ65604 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2004038335-A1.
PD 26-FEB-2004.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 393
ID ADM27740 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2004048333-A1.
PD 11-MAR-2004.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 394
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ID ADM17522 standard; protein; 344 AA.
DE Human secreted/transmembrane protein, PRO337.
PN US2004048332-A1.
PD 11-MAR-2004.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1806; DB 8; Length 344;
Pred. No. 5.3e-147;
RESULT 395
ID ADL07356 standard; protein; 344 AA.
DE Human secreted/transmembrane protein, PRO337.
PN US2004063921-A1.
PD 01-APR-2004.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1806; DB 8; Length 344;
Pred. No. 5.3e-147;
RESULT 396
ID ADM42464 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2004058424-A1.
PD 25-MAR-2004.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1806; DB 8; Length 344;
Pred. No. 5.3e-147;
RESULT 397
ID ADM28326 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2004077064-A1.
PD 22-APR-2004.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1806; DB 8; Length 344;
Pred. No. 5.3e-147;
RESULT 398
ID ADI95808 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003077659-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1806; DB 8; Length 344;
Pred. No. 5.3e-147;
RESULT 399
ID ADI96360 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003207354-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1806; DB 8; Length 344;
Pred. No. 5.3e-147;
RESULT 400
ID AD832312 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2004203125-A1.
PD 14-OCT-2004.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1806; DB 8; Length 344;
Pred. No. 5.3e-147;
RESULT 401
ID ADT03296 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2004214269-A1.
PD 28-OCT-2004.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1806; DB 8; Length 344;
Pred. No. 5.3e-147;
RESULT 402
ID ADU50478 standard; protein; 344 AA.
DE PRO337, SEQ ID 523.
PN US2004223964-A1.
PD 11-NOV-2004.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1806; DB 8; Length 344;
Pred. No. 5.3e-147;
RESULT 403
ID ADM49757 standard; protein; 344 AA.
DE PRO337 protein, SEQ ID 523.
PN US2005014226-A1.
PD 20-JAN-2005.
PA (ASHK/) ASHKENAZI A J.
PA (BAKE/) BAKER K P.
PA (BOTS/) BOTSTEIN D.
PA (DESN/) DESNOYERS L.
PA (EATO/) EATON D L.
PA (FERR/) FERRARA N.
PA (FILV/) FILVAROFF E.
PA (FONG/) FONG S.
PA (GAOW/) GAO W.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GRIM/) GRIMALDI J C.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (KLJA/) KLJAVIN I J.
PA (KUOS/) KUO S S.
PA (NAPI/) NAPIER M A.
PA (PANJ/) PAN J.
PA (PAON/) PAONI N F.
PA (ROYM/) ROY M A.
PA (SHEL/) SHELTON D L.
PA (STEW/) STEWART T A.
PA (TUMA/) TUMAS D.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match
Best Local Similarity 100.0%; Score 1806; DB 9; Length 344;
Pred. No. 5.3e-147;
RESULT 404
ID AD203347 standard; protein; 344 AA.
DE Human secreted/transmembrane protein PRO337.
PN US2005074837-A1.
PD 07-APR-2005.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1806; DB 9; Length 344;
Pred. No. 5.3e-147;
RESULT 405
ID AD252418 standard; protein; 344 AA.
DE Human secreted/transmembrane protein, PRO337.
PN US2005084935-A1.
PD 21-APR-2005.
PA (ASHK/) ASHKENAZI A J.
PA (BAKE/) BAKER K P.
PA (BOTS/) BOTSTEIN D.
PA (DESN/) DESNOYERS L.
PA (EATO/) EATON D L.
PA (FERR/) FERRARA N.
PA (FILV/) FILVAROFF E.
PA (FONG/) FONG S.
PA (GAOW/) GAO W.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GRIM/) GRIMALDI J C.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (KLJA/) KLJAVIN I J.
PA (KUOS/) KUO S S.
PA (NAPI/) NAPIER M A.
PA (PANJ/) PAN J.
PA (PAON/) PAONI N F.
PA (ROYM/) ROY M A.
PA (SHEL/) SHELTON D L.
PA (STEW/) STEWART T A.
PA (TUMA/) TUMAS D.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match
Best Local Similarity 100.0%; Score 1806; DB 9; Length 344;
Pred. No. 5.3e-147;

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Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 406
ID ABB14093 standard; protein; 344 AA.
DE Cancer cell diagnosis method-related human protein - SEQ ID 376.
PN US2005153396-A1.
PD 14-JUL-2005.
PA (BAKE/) BAKER K P.
PA (BERE/) BERSINI M.
PA (DEFO/) DEFORGE L.
PA (DESN/) DESNOYERS L.
PA (FILV/) FILVOROFF E.
PA (GAOW/) GAO W.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (SHER/) SHERWOOD S.
PA (SMIT/) SMITH V.
PA (STEW/) STEWART T A.
PA (TUMA/) TUMAS D.
PA (WATA/) WATANABE C K.
PA (WOOD/) WOOD W I.
PA (ZHAN/) ZHANG Z.
Query Match 100.0%; Score 1806; DB 9; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 407
ID AED48246 standard; protein; 344 AA.
DE Human PRO337 amino acid sequence.
PN US2005227342-A1.
PD 13-OCT-2005.
PA (GETH/) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 9; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 408
ID AED6291 standard; protein; 344 AA.
DE Human PRO amino acid sequence, seq id 376.
PN US2005245730-A1.
PD 03-NOV-2005.
PA (GETH/) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 9; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.3e-147;
RESULT 409
ID AAM40499 standard; protein; 355 AA.
DE Human polypeptide SEQ ID NO 5430.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 100.0%; Score 1806; DB 4; Length 355;
Best Local Similarity 100.0%; Pred. No. 5.5e-147;
RESULT 410
ID ADI21580 standard; protein; 355 AA.
DE Novel human polypeptide #59.
PN WO2003025148-A2.
PD 27-MAR-2003.
PA (HYSE-) HYSEQ INC.
Query Match 100.0%; Score 1806; DB 7; Length 355;
Best Local Similarity 100.0%; Pred. No. 5.5e-147;
RESULT 411
ID AAB19722 standard; protein; 344 AA.
DE Human SECX Clone 11753149.0.37-encoded protein.
PN WO200061754-A2.
PD 19-OCT-2000.
PA (CURA-) CURAGEN CORP.
Query Match 99.6%; Score 1799; DB 3; Length 344;
Best Local Similarity 99.7%; Pred. No. 2.1e-146;
RESULT 412
ID AAB19721 standard; protein; 344 AA.
DE Human SECX Clone 11753149.0.6-encoded protein.
PN WO200061754-A2.
PD 19-OCT-2000.
PA (CURA-) CURAGEN CORP.
Query Match 99.6%; Score 1799; DB 3; Length 344;
Best Local Similarity 99.7%; Pred. No. 2.1e-146;
RESULT 413
ID ADD18291 standard; protein; 344 AA.
DE Human molecule (MOL) protein MOL11.
PN WO2003003984-A2.
PD 16-JAN-2003.
PA (CURA-) CURAGEN CORP.
Query Match 99.6%; Score 1799; DB 7; Length 344;
Best Local Similarity 99.7%; Pred. No. 2.1e-146;
RESULT 414
ID ADD18289 standard; protein; 344 AA.
DE Human molecule (MOL) protein MOL10.
PN WO2003003984-A2.
PD 16-JAN-2003.
PA (CURA-) CURAGEN CORP.
Query Match 99.6%; Score 1799; DB 7; Length 344;
Best Local Similarity 99.7%; Pred. No. 2.1e-146;
RESULT 415
ID AAY41773 standard; protein; 343 AA.
DE Human PRO337 protein sequence.
PN WO9946281-A2.
PD 16-SEP-1999.
PA (GETH/) GENENTECH INC.
Query Match 99.2%; Score 1791.5; DB 2; Length 343;
Best Local Similarity 99.7%; Pred. No. 9.3e-146;
RESULT 416
ID RAM39713 standard; protein; 344 AA.
DE Human polypeptide SEQ ID NO 1858.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 92.2%; Score 1665.5; DB 4; Length 344;
Best Local Similarity 95.2%; Pred. No. 6.9e-135;
RESULT 417
ID ABJ20227 standard; protein; 344 AA.
DE Human IG gene related protein SEQ ID NO 50.
PN WO200299040-A2.
PD 12-DEC-2002.
PA (EXEL-) EXELIXIS INC.
Query Match 92.2%; Score 1665.5; DB 6; Length 344;
Best Local Similarity 95.2%; Pred. No. 6.9e-135;
RESULT 418
ID ABU56719 standard; protein; 344 AA.
DE Lung cancer-associated polypeptide #312.
PN WO200286443-A2.
PD 31-OCT-2002.
PA (BOSB-) EOS BIOTECHNOLOGY INC.
Query Match 92.2%; Score 1665.5; DB 6; Length 344;
Best Local Similarity 95.2%; Pred. No. 6.9e-135;
RESULT 419
ID ADG63209 standard; protein; 344 AA.
DE Human neurotrophin protein.
PN WO2003002765-A2.
PD 09-JAN-2003.
PA (IMCR-) IMPERIAL CANCER RES TECHNOLOGY LTD.
Query Match 92.2%; Score 1665.5; DB 7; Length 344;
Best Local Similarity 95.2%; Pred. No. 6.9e-135;
RESULT 420
ID ADN39138 standard; protein; 344 AA.
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:456.
PN WO2003042661-A2.
PD 22-MAY-2003.
PA (BOSB-) EOS BIOTECHNOLOGY INC.
Query Match 92.2%; Score 1665.5; DB 7; Length 344;
Best Local Similarity 95.2%; Pred. No. 6.9e-135;
RESULT 421
ID ADG63211 standard; protein; 355 AA.
DE Human neurotrophin protein +33bp isoform.
PN WO2003002765-A2.
PD 09-JAN-2003.
PA (IMCR-) IMPERIAL CANCER RES TECHNOLOGY LTD.
Query Match 91.4%; Score 1650; DB 7; Length 355;
Best Local Similarity 92.2%; Pred. No. 1.6e-133;
RESULT 422

ID ADI35770 standard; protein; 355 AA.
DE Human neurotrophin.
PN US2003100485-A1.
PD 29-MAY-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 91.4%; Score 1650; DB 7; Length 355;
Best Local Similarity 92.2%; Pred. No. 1.6e-133;
RESULT 423
ID ADG63213 standard; protein; 367 AA.
DE Human neurotrophin protein +69bp isoform.
PN WO2003002765-A2.
PD 09-JAN-2003.
PA (IMCR) IMPERIAL CANCER RES TECHNOLOGY LTD.
Query Match 91.0%; Score 1644; DB 7; Length 367;
Best Local Similarity 89.1%; Pred. No. 5.4e-133;
RESULT 424
ID AAU79205 standard; protein; 381 AA.
DE Human Kruppel associated DNA binding protein 42.
PN WO200183541-A1.
PD 08-NOV-2001.
PA (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.
Query Match 91.0%; Score 1643; DB 5; Length 381;
Best Local Similarity 98.7%; Pred. No. 6.9e-133;
RESULT 425
ID AAY57602 standard; protein; 313 AA.
DE Human protein SEQ ID NO.4.
PN WO95958668-A1.
PD 18-NOV-1999.
PA (ONOF) ONO PHARM CO LTD.
Query Match 90.9%; Score 1642; DB 3; Length 313;
Best Local Similarity 100.0%; Pred. No. 6.5e-133;
RESULT 426
ID ADI35772 standard; protein; 344 AA.
DE Rat neurotrophin.
PN US2003100485-A1.
PD 29-MAY-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 90.8%; Score 1639.5; DB 7; Length 344;
Best Local Similarity 92.9%; Pred. No. 1.2e-132;
RESULT 427
ID ADG63215 standard; protein; 376 AA.
DE Human neurotrophin protein +108bp isoform.
PN WO2003002765-A2.
PD 09-JAN-2003.
PA (IMCR) IMPERIAL CANCER RES TECHNOLOGY LTD.
Query Match 90.8%; Score 1639.5; DB 7; Length 376;
Best Local Similarity 87.0%; Pred. No. 1.4e-132;
RESULT 428
ID ADE07928 standard; protein; 338 AA.
DE Novel protein (useful for identifying genetic disorders) #83.
PN WO2003054152-A2.
PD 03-JUL-2003.
PA (HYSE-) HYSEQ INC.
Query Match 71.7%; Score 1295.5; DB 7; Length 338;
Best Local Similarity 71.6%; Pred. No. 5.5e-103;
RESULT 429
ID ADO47380 standard; protein; 250 AA.
DE Human neurotrophin-like protein-related rat neurotrophin protein SeqID15.
PN WO2004039942-A2.
PD 13-MAY-2004.
PA (NUVE-) NUVELO.
Query Match 71.7%; Score 1295; DB 8; Length 250;
Best Local Similarity 97.6%; Pred. No. 4e-103;
RESULT 430
ID ABJ20236 standard; protein; 345 AA.
DE Human IG gene related protein SEQ ID No 59.
PN WO200299040-A2.
PD 12-DEC-2002.
PA (EXEL-) EXELIXIS INC.
Query Match 70.2%; Score 1268; DB 6; Length 345;
Best Local Similarity 71.2%; Pred. No. 1.3e-100;
RESULT 431
ID ADE83448 standard; protein; 345 AA.

DE Human Protein Q14982, SEQ ID NO 11043.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO-) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 70.2%; Score 1268; DB 7; Length 345;
Best Local Similarity 71.2%; Pred. No. 1.3e-100;
RESULT 432
ID ADG63207 standard; protein; 345 AA.
DE Opioid-binding protein/cell adhesion molecule-like protein.
PN WO2003002765-A2.
PD 09-JAN-2003.
PA (IMCR) IMPERIAL CANCER RES TECHNOLOGY LTD.
Query Match 70.2%; Score 1268; DB 7; Length 345;
Best Local Similarity 71.2%; Pred. No. 1.3e-100;
RESULT 433
ID ADV73205 standard; protein; 345 AA.
DE Human colon tumor cell upregulated protein SEQ ID NO 46.
PN WO2004110345-A2.
PD 23-DEC-2004.
PA (PHAA) PHARMACIA CORP.
Query Match 70.2%; Score 1268; DB 9; Length 345;
Best Local Similarity 71.2%; Pred. No. 1.3e-100;
RESULT 434
ID ADE83446 standard; protein; 345 AA.
DE Rat Protein P32736, SEQ ID NO 11041.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 69.7%; Score 1259; DB 7; Length 345;
Best Local Similarity 71.2%; Pred. No. 8e-100;
RESULT 435
ID AAOL9641 standard; protein; 335 AA.
DE Human limbic system associated membrane protein 36-85.
PN CN1345756-A.
PD 24-APR-2002.
PA (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.
Query Match 51.6%; Score 932.5; DB 5; Length 335;
Best Local Similarity 53.9%; Pred. No. 1.1e-71;
RESULT 436
ID ABJ20235 standard; protein; 338 AA.
DE Human IG gene related protein SEQ ID No 58.
PN WO200299040-A2.
PD 12-DEC-2002.
PA (EXEL-) EXELIXIS INC.
Query Match 51.6%; Score 931.5; DB 6; Length 338;
Best Local Similarity 55.4%; Pred. No. 1.4e-71;
RESULT 437
ID ADL12675 standard; protein; 338 AA.
DE Human steroid-induced C3A liver cell protein #60.
PN US6673549-B1.
PD 06-JAN-2004.
PA (INCY-) INCYTE CORP.
Query Match 51.6%; Score 931.5; DB 8; Length 338;
Best Local Similarity 55.4%; Pred. No. 1.4e-71;
RESULT 438
ID ADX26265 standard; protein; 338 AA.
DE Novel cell pain response detection method-related human protein SeqID611.
PN WO2005014849-A2.
PD 17-FEB-2005.
PA (EURO-) EUROCELTIQUE SA.
Query Match 51.6%; Score 931.5; DB 9; Length 338;
Best Local Similarity 55.4%; Pred. No. 1.4e-71;
RESULT 439
ID AAOW05153 standard; protein; 338 AA.
DE Rat LAMP residues 1-332.
PN WO9630052-A1.
PD 03-OCT-1996.
PA (UMDN-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.
Query Match 51.3%; Score 926.5; DB 2; Length 338;
Best Local Similarity 55.1%; Pred. No. 3.7e-71;
RESULT 440

ID AAW05154 standard; protein; 338 AA.
DE Rat LAMP residues 1-332.
PN WO9630052-A1.
PD 03-OCT-1996.
PA (UMDNJ-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.
Query Match 51.3%; Score 926.5; DB 2; Length 338;
Best Local Similarity 55.1%; Pred. No. 3.7e-71;
RESULT 441
ID ADX26409 standard; protein; 338 AA.
DE Novel cell pain response detection method-related rat protein SeqID755.
PN WO2005014849-A2.
PD 17-FEB-2005.
PA (EURO-) EUROCELTIQUE SA.
Query Match 49.4%; Score 893; DB 6; Length 383;
Best Local Similarity 53.3%; Pred. No. 3.4e-68;
RESULT 442
ID AEA26105 standard; protein; 334 AA.
DE Human renal cell carcinoma-related LSAMP protein SeqID125.
PN WO2005047519-A2.
PD 26-MAY-2005.
PA (VAND-) VAN ANDEL RES INST.
Query Match 51.2%; Score 925.5; DB 9; Length 334;
Best Local Similarity 55.3%; Pred. No. 4.5e-71;
RESULT 443
ID AAW05152 standard; protein; 325 AA.
DE Human LAMP residues 8-332.
PN WO9630052-A1.
PD 03-OCT-1996.
PA (UMDNJ-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.
Query Match 51.1%; Score 923.5; DB 2; Length 325;
Best Local Similarity 55.3%; Pred. No. 6.4e-71;
RESULT 444
ID AAW05172 standard; protein; 361 AA.
DE Rat LAMP clone 6c.
PN WO9630052-A1.
PD 03-OCT-1996.
PA (UMDNJ-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.
Query Match 50.6%; Score 913; DB 2; Length 361;
Best Local Similarity 51.7%; Pred. No. 6e-70;
RESULT 445
ID AAW05157 standard; protein; 308 AA.
DE Human LAMP residues 8-315.
PN WO9630052-A1.
PD 03-OCT-1996.
PA (UMDNJ-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.
Query Match 50.3%; Score 908; DB 2; Length 308;
Best Local Similarity 56.3%; Pred. No. 1.3e-69;
RESULT 446
ID AAW05158 standard; protein; 315 AA.
DE Rat LAMP residues 1-315.
PN WO9630052-A1.
PD 03-OCT-1996.
PA (UMDNJ-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.
Query Match 50.2%; Score 907; DB 2; Length 315;
Best Local Similarity 56.3%; Pred. No. 1.6e-69;
RESULT 447
ID AAW05156 standard; protein; 310 AA.
DE Rat mature LAMP.
PN WO9630052-A1.
PD 03-OCT-1996.
PA (UMDNJ-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.
Query Match 50.1%; Score 905; DB 2; Length 310;
Best Local Similarity 55.3%; Pred. No. 2.4e-69;
RESULT 448
ID AAW05155 standard; protein; 304 AA.
DE Human mature LAMP.
PN WO9630052-A1.
PD 03-OCT-1996.
PA (UMDNJ-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.
Query Match 49.9%; Score 902; DB 2; Length 304;
Best Local Similarity 55.5%; Pred. No. 4.2e-69;
RESULT 449
ID ADX26335 standard; protein; 341 AA.

DE Novel cell pain response detection method-related mouse protein SeqID681.
PN WO2005014849-A2.
PD 17-FEB-2005.
PA (EURO-) EUROCELTIQUE SA.
Query Match 49.5%; Score 894; DB 9; Length 341;
Best Local Similarity 56.3%; Pred. No. 2.4e-68;
RESULT 450
ID ABR39441 standard; protein; 383 AA.
DE Human GENSET polypeptide clone name SLAMP.
PN WO2003014151-A2.
PD 20-FEB-2003.
PA (GEST) GENSET SA.
Query Match 49.4%; Score 893; DB 6; Length 383;
Best Local Similarity 53.3%; Pred. No. 3.4e-68;
RESULT 451
ID AAW05159 standard; protein; 287 AA.
DE Human LAMP residues 29-315.
PN WO9630052-A1.
PD 03-OCT-1996.
PA (UMDNJ-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.
Query Match 49.1%; Score 886.5; DB 2; Length 287;
Best Local Similarity 56.6%; Pred. No. 8.4e-68;
RESULT 452
ID AAW05160 standard; protein; 287 AA.
DE Rat LAMP residues 29-315.
PN WO9630052-A1.
PD 03-OCT-1996.
PA (UMDNJ-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.
Query Match 49.0%; Score 885.5; DB 2; Length 287;
Best Local Similarity 56.6%; Pred. No. 1e-67;
RESULT 453
ID ADM47275 standard; protein; 203 AA.
DE Oestrogen regulated protein like NOVX 25b protein.
PN WO2003083039-A2.
PD 09-OCT-2003.
PA (CURA-) CURAGEN CORP.
Query Match 48.4%; Score 873.5; DB 7; Length 203;
Best Local Similarity 54.5%; Pred. No. 6.9e-67;
RESULT 454
ID AAG75020 standard; protein; 326 AA.
DE Human colon cancer antigen protein Seq ID NO:5784.
PN WO200122920-A2.
PD 05-APR-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 47.2%; Score 852.5; DB 4; Length 326;
Best Local Similarity 51.6%; Pred. No. 8.6e-65;
RESULT 455
ID AAB31212 standard; protein; 354 AA.
DE Amino acid sequence of human polypeptide PRO6004.
PN WO200077037-A2.
PD 21-DEC-2000.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 4; Length 354;
Best Local Similarity 47.9%; Pred. No. 3.4e-62;
RESULT 456
ID ABP53580 standard; protein; 354 AA.
DE Human NOViza protein Seq ID NO:24.
PN WO200262999-A2.
PD 15-AUG-2002.
PA (CURA-) CURAGEN CORP.
Query Match 45.6%; Score 823; DB 5; Length 354;
Best Local Similarity 47.9%; Pred. No. 3.4e-62;
RESULT 457
ID AAU83592 standard; protein; 354 AA.
DE Human PRO protein, Seq ID NO 2.
PN WO200208288-A2.
PD 31-JAN-2002.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 5; Length 354;
Best Local Similarity 47.9%; Pred. No. 3.4e-62;
RESULT 458
ID ADI28023 standard; protein; 354 AA.
DE ECMCAD protein 7087904CD1.

PN WO200202634-A2.
PD 10-JAN-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 45.6%; Score 823; DB 5; Length 354;
Best Local Similarity 47.9%; Pred. No. 3.4e-62;
RESULT 459
ID ADY311742 standard; protein; 354 AA.
DE Novel human secreted and transmembrane protein PRO6004.
PN WO200193983-A1.
PD 13-DEC-2001.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 5; Length 354;
Best Local Similarity 47.9%; Pred. No. 3.4e-62;
RESULT 460
ID ABU80739 standard; protein; 354 AA.
DE Human PRO polypeptide #1.
PN US2003036835-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 6; Length 354;
Best Local Similarity 47.9%; Pred. No. 3.4e-62;
RESULT 461
ID ABO25183 standard; protein; 354 AA.
DE Novel human secreted and transmembrane protein PRO6004.
PN US2003040014-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 6; Length 354;
Best Local Similarity 47.9%; Pred. No. 3.4e-62;
RESULT 462
ID ABO33705 standard; protein; 354 AA.
DE Novel human secreted and transmembrane protein PRO6004.
PN US2003045687-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 6; Length 354;
Best Local Similarity 47.9%; Pred. No. 3.4e-62;
RESULT 463
ID ABU67301 standard; protein; 354 AA.
DE Novel human secreted and transmembrane protein PRO6004.
PN US2003032063-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 6; Length 354;
Best Local Similarity 47.9%; Pred. No. 3.4e-62;
RESULT 464
ID ABU72069 standard; protein; 354 AA.
DE Novel human secreted and transmembrane protein PRO6004.
PN US2002177165-A1.
PD 28-NOV-2002.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 6; Length 354;
Best Local Similarity 47.9%; Pred. No. 3.4e-62;
RESULT 465
ID ABU67170 standard; protein; 354 AA.
DE Novel human secreted and transmembrane protein PRO6004.
PN US2003032062-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 6; Length 354;
Best Local Similarity 47.9%; Pred. No. 3.4e-62;
RESULT 466
ID ABU82048 standard; protein; 354 AA.
DE Novel human secreted and transmembrane protein PRO6004.
PN US2003080863-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 6; Length 354;
Best Local Similarity 47.9%; Pred. No. 3.4e-62;
RESULT 467
ID ABU79812 standard; protein; 354 AA.
DE Human secreted/transmembrane protein PRO6004.
PN US2003032057-A1.

PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 6; Length 354;
Best Local Similarity 47.9%; Pred. No. 3.4e-62;
RESULT 468
ID ABJ72228 standard; protein; 354 AA.
DE Human PRO6004 protein.
PN US2003050448-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 6; Length 354;
Best Local Similarity 47.9%; Pred. No. 3.4e-62;
RESULT 469
ID ADA47302 standard; protein; 354 AA.
DE Human secreted/transmembrane polypeptide PRO6004.
PN US2003044844-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 6; Length 354;
Best Local Similarity 47.9%; Pred. No. 3.4e-62;
RESULT 470
ID ABJ72356 standard; protein; 354 AA.
DE Human PRO6004 protein.
PN US2003027988-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 6; Length 354;
Best Local Similarity 47.9%; Pred. No. 3.4e-62;
RESULT 471
ID ABO34251 standard; protein; 354 AA.
DE Human secreted/transmembrane polypeptide PRO 6004.
PN US2003044934-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 6; Length 354;
Best Local Similarity 47.9%; Pred. No. 3.4e-62;
RESULT 472
ID ABO19870 standard; protein; 354 AA.
DE Human secreted/transmembrane protein PRO6004.
PN US2003044902-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 7; Length 354;
Best Local Similarity 47.9%; Pred. No. 3.4e-62;
RESULT 473
ID ABJ72058 standard; protein; 354 AA.
DE Human membrane bound receptor/protein PRO6004 amino acid sequence.
PN US2003065147-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 7; Length 354;
Best Local Similarity 47.9%; Pred. No. 3.4e-62;
RESULT 474
ID ADB83492 standard; protein; 354 AA.
DE Novel human secreted and transmembrane protein PRO6004.
PN US2003073814-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 7; Length 354;
Best Local Similarity 47.9%; Pred. No. 3.4e-62;
RESULT 475
ID ADB80598 standard; protein; 354 AA.
DE Novel human secreted and transmembrane protein PRO6004.
PN US2003080868-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 7; Length 354;
Best Local Similarity 47.9%; Pred. No. 3.4e-62;
RESULT 476
ID ADB73139 standard; protein; 354 AA.
DE Novel human secreted and transmembrane protein PRO6004.
PN US2003096968-A1.
PD 22-MAY-2003.

Query Match	45.6%;	Score 823;	DB 7;	Length 354;
Best Local Similarity	47.9%;	Pred. No. 3.4e-62;		
RESULT 486				
ID ADC49752 standard; protein; 354 AA.				
DE Novel human secreted and transmembrane protein PRO6004.				
FN US200308064-A1.				
PD 08-MAY-2003.				
PA (GETH) GENENTECH INC.				
Query Match	45.6%;	Score 823;	DB 7;	Length 354;
Best Local Similarity	47.9%;	Pred. No. 3.4e-62;		
RESULT 487				
ID ADC48951 standard; protein; 354 AA.				
DE Novel human secreted and transmembrane protein PRO6004.				
FN US2003088070-A1.				
PD 08-MAY-2003.				
PA (GETH) GENENTECH INC.				
Query Match	45.6%;	Score 823;	DB 7;	Length 354;
Best Local Similarity	47.9%;	Pred. No. 3.4e-62;		
RESULT 488				
ID ADC49468 standard; protein; 354 AA.				
DE Novel human secreted and transmembrane protein PRO6004.				
FN US2003088071-A1.				
PD 08-MAY-2003.				
PA (GETH) GENENTECH INC.				
Query Match	45.6%;	Score 823;	DB 7;	Length 354;
Best Local Similarity	47.9%;	Pred. No. 3.4e-62;		
RESULT 489				
ID ADC47329 standard; protein; 354 AA.				
DE Novel human secreted and transmembrane protein PRO6004.				
FN US2003088072-A1.				
PD 08-MAY-2003.				
PA (GETH) GENENTECH INC.				
Query Match	45.6%;	Score 823;	DB 7;	Length 354;
Best Local Similarity	47.9%;	Pred. No. 3.4e-62;		
RESULT 490				
ID ADC47074 standard; protein; 354 AA.				
DE Novel human secreted and transmembrane protein PRO6004.				
FN US2003105288-A1.				
PD 05-JUN-2003.				
PA (GETH) GENENTECH INC.				
Query Match	45.6%;	Score 823;	DB 7;	Length 354;
Best Local Similarity	47.9%;	Pred. No. 3.4e-62;		
RESULT 491				
ID ADC77949 standard; protein; 354 AA.				
DE Novel human secreted and transmembrane protein PRO6004.				
FN US2003098572-A1.				
PD 22-MAY-2003.				
PA (GETH) GENENTECH INC.				
Query Match	45.6%;	Score 823;	DB 7;	Length 354;
Best Local Similarity	47.9%;	Pred. No. 3.4e-62;		
RESULT 492				
ID ADD06184 standard; protein; 354 AA.				
DE Novel human secreted and transmembrane protein PRO6004.				
FN US2003073816-A1.				
PD 17-APR-2003.				
PA (GETH) GENENTECH INC.				
Query Match	45.6%;	Score 823;	DB 7;	Length 354;
Best Local Similarity	47.9%;	Pred. No. 3.4e-62;		
RESULT 493				
ID ADC77703 standard; protein; 354 AA.				
DE Novel human secreted and transmembrane protein PRO6004.				
FN US2003088066-A1.				
PD 08-MAY-2003.				
PA (GETH) GENENTECH INC.				
Query Match	45.6%;	Score 823;	DB 7;	Length 354;
Best Local Similarity	47.9%;	Pred. No. 3.4e-62;		
RESULT 494				
ID ADD50666 standard; protein; 354 AA.				
DE Novel human secreted and transmembrane protein PRO6004.				
FN US2003105291-A1.				
PD 05-JUN-2003.				
PA (GETH) GENENTECH INC.				
Query Match	45.6%;	Score 823;	DB 7;	Length 354;
Best Local Similarity	47.9%;	Pred. No. 3.4e-62;		
RESULT 495				
ID ADC77703 standard; protein; 354 AA.				
DE Novel human secreted and transmembrane protein PRO6004.				
FN US2003088066-A1.				
PD 08-MAY-2003.				
PA (GETH) GENENTECH INC.				
Query Match	45.6%;	Score 823;	DB 7;	Length 354;
Best Local Similarity	47.9%;	Pred. No. 3.4e-62;		
RESULT 496				
ID ADC77703 standard; protein; 354 AA.				
DE Novel human secreted and transmembrane protein PRO6004.				
FN US2003088066-A1.				
PD 08-MAY-2003.				
PA (GETH) GENENTECH INC.				
Query Match	45.6%;	Score 823;	DB 7;	Length 354;
Best Local Similarity	47.9%;	Pred. No. 3.4e-62;		
RESULT 497				
ID ADC77703 standard; protein; 354 AA.				
DE Novel human secreted and transmembrane protein PRO6004.				
FN US2003088066-A1.				
PD 08-MAY-2003.				
PA (GETH) GENENTECH INC.				
Query Match	45.6%;	Score 823;	DB 7;	Length 354;
Best Local Similarity	47.9%;	Pred. No. 3.4e-62;		

Best Local Similarity 47.9%; Pred. No. 3.4e-62;
RESULT 495
ID ADD50912 standard; protein; 354 AA.
DE Novel human secreted and transmembrane protein PRO6004.
PN US2003105290-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 7; Length 354;
Best Local Similarity 47.9%; Pred. No. 3.4e-62;
RESULT 496
ID ADD50393 standard; protein; 354 AA.
DE Human PRO polypeptide #1.
PN US2003096971-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 7; Length 354;
Best Local Similarity 47.9%; Pred. No. 3.4e-62;
RESULT 497
ID ADD50147 standard; protein; 354 AA.
DE Human PRO polypeptide #1.
PN US2003096970-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 7; Length 354;
Best Local Similarity 47.9%; Pred. No. 3.4e-62;
RESULT 498
ID ADD51158 standard; protein; 354 AA.
DE Novel human secreted and transmembrane protein PRO6004.
PN US2003105289-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 7; Length 354;
Best Local Similarity 47.9%; Pred. No. 3.4e-62;
RESULT 499
ID ADG63811 standard; protein; 354 AA.
DE Human secreted/transmembrane polypeptide PRO6004.
PN US2003170721-A1.
PD 11-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 7; Length 354;
Best Local Similarity 47.9%; Pred. No. 3.4e-62;
RESULT 500
ID ADC48705 standard; protein; 354 AA.
DE Novel human secreted and transmembrane protein PRO6004.
PN US2003092888-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 3.4e-62;
RESULT 501
ID ADE20876 standard; protein; 354 AA.
DE Novel human secreted and transmembrane protein PRO6004.
PN US2003100735-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 3.4e-62;
RESULT 502
ID ADR05720 standard; protein; 354 AA.
DE Human PRO polypeptide #1.
PN US2003100728-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 3.4e-62;
RESULT 503
ID ADD74949 standard; protein; 354 AA.
DE Human PRO polypeptide #1.
PN US2003100712-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 3.4e-62;
RESULT 504
ID ADD75695 standard; protein; 354 AA.
DE Novel human secreted and transmembrane protein PRO6004.
PN US2003100717-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 3.4e-62;
RESULT 505
ID ADD84927 standard; protein; 354 AA.
DE Novel human secreted and transmembrane protein PRO6004.
PN US2003100722-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 3.4e-62;
RESULT 506
ID ADD86753 standard; protein; 354 AA.
DE Novel human secreted and transmembrane protein PRO6004.
PN US2003100738-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 3.4e-62;
RESULT 507
ID ADE20630 standard; protein; 354 AA.
DE Novel human secreted and transmembrane protein PRO6004.
PN US2003100734-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 3.4e-62;
RESULT 508
ID ADE38927 standard; protein; 354 AA.
DE Novel human secreted and transmembrane protein PRO6004.
PN US2003096362-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 3.4e-62;
RESULT 509
ID ADE05474 standard; protein; 354 AA.
DE Human PRO polypeptide #1.
PN US2003100727-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 3.4e-62;
RESULT 510
ID ADD73459 standard; protein; 354 AA.
DE Human PRO polypeptide #1.
PN US2003100711-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 3.4e-62;
RESULT 511
ID ADD78299 standard; protein; 354 AA.
DE Novel human secreted and transmembrane protein PRO6004.
PN US2003100737-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 3.4e-62;
RESULT 512
ID ADE21122 standard; protein; 354 AA.
DE Novel human secreted and transmembrane protein PRO6004.
PN US2003100736-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 3.4e-62;
RESULT 513
ID ADE21122 standard; protein; 354 AA.
DE Novel human secreted and transmembrane protein PRO6004.
PN US2003100736-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 3.4e-62;

ID ADD77237 standard; protein; 354 AA.
DE Novel human secreted and transmembrane protein PRO6004.
PN US2003100732-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 3.4e-62;
RESULT 514
ID ADE20384 standard; protein; 354 AA.
DE Novel human secreted and transmembrane protein PRO6004.
PN US2003100733-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 3.4e-62;
RESULT 515
ID ADD75449 standard; protein; 354 AA.
DE Human PRO polypeptide #1.
PN US2003100064-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 3.4e-62;
RESULT 516
ID ADD73965 standard; protein; 354 AA.
DE Human PRO polypeptide #1.
PN US2003100708-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 3.4e-62;
RESULT 517
ID ADD74211 standard; protein; 354 AA.
DE Human PRO polypeptide #1.
PN US2003100709-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 3.4e-62;
RESULT 518
ID ADD75941 standard; protein; 354 AA.
DE Novel human secreted and transmembrane protein PRO6004.
PN US2003100718-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 3.4e-62;
RESULT 519
ID ADD85433 standard; protein; 354 AA.
DE Novel human secreted and transmembrane protein PRO6004.
PN US2003100721-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 3.4e-62;
RESULT 520
ID ADE04982 standard; protein; 354 AA.
DE Human PRO polypeptide #1.
PN US2003100726-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 3.4e-62;
RESULT 521
ID ADD75195 standard; protein; 354 AA.
DE Human PRO polypeptide #1.
PN US2003100714-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 3.4e-62;
RESULT 522
ID ADD76739 standard; protein; 354 AA.
DE Novel human secreted and transmembrane protein PRO6004.
PN US2003100715-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 3.4e-62;
RESULT 523
ID ADD86507 standard; protein; 354 AA.
DE Novel human secreted and transmembrane protein PRO6004.
PN US2003100719-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 3.4e-62;
RESULT 524
ID ADE41225 standard; protein; 354 AA.
DE Human secreted/transmembrane polypeptide PRO6004.
PN US2003104558-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 3.4e-62;
RESULT 525
ID ADD77975 standard; protein; 354 AA.
DE Novel human secreted and transmembrane protein PRO6004.
PN US2003100731-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 3.4e-62;
RESULT 526
ID ADD77483 standard; protein; 354 AA.
DE Novel human secreted and transmembrane protein PRO6004.
PN US2003100729-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 3.4e-62;
RESULT 527
ID ADD77729 standard; protein; 354 AA.
DE Novel human secreted and transmembrane protein PRO6004.
PN US2003100730-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 3.4e-62;
RESULT 528
ID ADD85187 standard; protein; 354 AA.
DE Novel human secreted and transmembrane protein PRO6004.
PN US2003100725-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 3.4e-62;
RESULT 529
ID ADD73719 standard; protein; 354 AA.
DE Human PRO polypeptide #1.
PN US2003100710-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 3.4e-62;
RESULT 530
ID ADD74457 standard; protein; 354 AA.
DE Human PRO polypeptide #1.
PN US2003100713-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 3.4e-62;
RESULT 531
ID ADD76985 standard; protein; 354 AA.
DE Novel human secreted and transmembrane protein PRO6004.

PN US2003100716-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 3.4e-62;
RESULT 532
ID ADH85679 standard; protein; 354 AA.
DE Novel human secreted and transmembrane protein PRO6004.
PN US2003100720-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 3.4e-62;
RESULT 533
ID ADE05228 standard; protein; 354 AA.
DE Human PRO polypeptide #1.
PN US2003100723-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 3.4e-62;
RESULT 534
ID ADD74703 standard; protein; 354 AA.
DE Human PRO polypeptide #1.
PN US2003100724-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 3.4e-62;
RESULT 535
ID ADG05515 standard; protein; 354 AA.
DE Novel human secreted and transmembrane protein PRO6004.
PN US2003096959-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 3.4e-62;
RESULT 536
ID ADG27069 standard; protein; 354 AA.
DE Human PRO polypeptide #1.
PN US2003096962-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 3.4e-62;
RESULT 537
ID ADG11132 standard; protein; 354 AA.
DE Novel human secreted and transmembrane protein PRO6004.
PN US2003096967-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 3.4e-62;
RESULT 538
ID ADG11911 standard; protein; 354 AA.
DE Novel human secreted and transmembrane protein PRO6004.
PN US2003096963-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 3.4e-62;
RESULT 539
ID ADP94468 standard; protein; 354 AA.
DE Novel human secreted and transmembrane protein PRO6004.
PN US2003096964-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 3.4e-62;
RESULT 540
ID ADG06564 standard; protein; 354 AA.
DE Human PRO polypeptide #1.
PN US2003096966-A1.

PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 3.4e-62;
RESULT 541
ID ADH38908 standard; protein; 354 AA.
DE Novel human secreted and transmembrane protein PRO6004.
PN US2003096965-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 3.4e-62;
RESULT 542
ID ADG63659 standard; protein; 354 AA.
DE Human secreted/transmembrane polypeptide PRO6004.
PN US2003180796-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 3.4e-62;
RESULT 543
ID ADG33998 standard; protein; 354 AA.
DE Novel human secreted and transmembrane protein PRO6004.
PN US2004006206-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 3.4e-62;
RESULT 544
ID ADI33468 standard; protein; 354 AA.
DE Human PRO polypeptide #1.
PN US2003096960-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 3.4e-62;
RESULT 545
ID ADH69562 standard; protein; 354 AA.
DE Human PRO polypeptide #1.
PN US2004019183-A1.
PD 29-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 3.4e-62;
RESULT 546
ID ADI29723 standard; protein; 354 AA.
DE Novel human secreted and transmembrane protein PRO6004.
PN US2003096961-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 3.4e-62;
RESULT 547
ID ADM27120 standard; protein; 354 AA.
DE Novel human secreted and transmembrane protein PRO6004.
PN US2004044179-A1.
PD 04-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 3.4e-62;
RESULT 548
ID ADK66478 standard; protein; 354 AA.
DE Human PRO polypeptide #1.
PN US2004044180-A1.
PD 04-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 3.4e-62;
RESULT 549
ID ADS82050 standard; protein; 354 AA.
DE Human cancer-associated protein #5.
PN WO2004035789-A1.
PD 29-APR-2004.

PA (GLDS) LG LIFE SCI LTD.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 3.4e-62;
RESULT 550
ID ABB98407 standard; protein; 354 AA.
DE Human NOV6, KILON-like protein.
PN W0200255704-A2.
PD 18-JUL-2002.
PA (CURA-) CURAGEN CORP.
Query Match 45.5%; Score 822; DB 5; Length 354;
Best Local Similarity 47.9%; Pred. No. 4.1e-62;
RESULT 551
ID ADB64811 standard; protein; 354 AA.
DE Human protein encoded by clone OCBPF20110210.
PN EP1308459-A2.
PD 07-MAY-2003.
PA (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 45.4%; Score 820; DB 7; Length 354;
Best Local Similarity 47.9%; Pred. No. 6.1e-62;
RESULT 552
ID ABP53581 standard; protein; 354 AA.
DE Human NOV12b protein SEQ ID NO:36.
PN W0200262999-A2.
PD 15-AUG-2002.
PA (CURA-) CURAGEN CORP.
Query Match 45.3%; Score 819; DB 5; Length 354;
Best Local Similarity 48.6%; Pred. No. 7.4e-62;
RESULT 553
ID ABU20234 standard; protein; 348 AA.
DE Human IG gene related protein SEQ ID NO 57.
PN W0200299040-A2.
PD 12-DEC-2002.
PA (EXEL-) EXELIXIS INC.
Query Match 45.1%; Score 815; DB 6; Length 348;
Best Local Similarity 47.5%; Pred. No. 1.6e-61;
RESULT 554
ID ABU20233 standard; protein; 348 AA.
DE Human IG gene related protein SEQ ID NO 56.
PN W0200299040-A2.
PD 12-DEC-2002.
PA (EXEL-) EXELIXIS INC.
Query Match 45.1%; Score 815; DB 6; Length 348;
Best Local Similarity 47.5%; Pred. No. 1.6e-61;
RESULT 555
ID AAB44331 standard; protein; 352 AA.
DE Human PRO4993 protein sequence SEQ ID NO:612.
PN W0200053756-A2.
PD 14-SEP-2000.
PA (GETH) GENENTECH INC.
Query Match 45.1%; Score 815; DB 3; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.6e-61;
RESULT 556
ID ABO25277 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO4993.
PN US2003050239-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 45.1%; Score 815; DB 6; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.6e-61;
RESULT 557
ID ABU72283 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO4993.
PN US2002192706-A1.
PD 19-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 45.1%; Score 815; DB 6; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.6e-61;
RESULT 558
ID ABU09489 standard; protein; 352 AA.
DE Human secreted and transmembrane PRO polypeptide #39.
PN US2002177553-A1.
PD 28-NOV-2002.

PA (GETH) GENENTECH INC.
Query Match 45.1%; Score 815; DB 6; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.6e-61;
RESULT 559
ID ABU61161 standard; protein; 352 AA.
DE Human PRO4993 polypeptide.
PN US2002169284-A1.
PD 14-NOV-2002.
PA (GETH) GENENTECH INC.
Query Match 45.1%; Score 815; DB 6; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.6e-61;
RESULT 560
ID ABU80430 standard; protein; 352 AA.
DE Human secreted/transmembrane protein PRO4993.
PN US2003004102-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 45.1%; Score 815; DB 6; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.6e-61;
RESULT 561
ID ADA25150 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO4993.
PN US2003050241-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 45.1%; Score 815; DB 6; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.6e-61;
RESULT 562
ID ABO19732 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO4993.
PN US2003050240-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 45.1%; Score 815; DB 6; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.6e-61;
RESULT 563
ID ADA12812 standard; protein; 352 AA.
DE Human secreted/transmembrane polypeptide PRO4993.
PN US2003055216-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 45.1%; Score 815; DB 6; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.6e-61;
RESULT 564
ID ABO19623 standard; protein; 352 AA.
DE Novel human secreted and transmembrane polypeptide #91.
PN US2003049633-A1.
PD 13-MAR-2003.
Query Match 45.1%; Score 815; DB 6; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.6e-61;
RESULT 565
ID ADB74118 standard; protein; 352 AA.
DE Human PRO polypeptide #91.
PN US2003045462-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 45.1%; Score 815; DB 7; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.6e-61;
RESULT 566
ID ADB76834 standard; protein; 352 AA.
DE Human PRO polypeptide #91.
PN US2003083248-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.1%; Score 815; DB 7; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.6e-61;
RESULT 567
ID ADC44260 standard; protein; 352 AA.
DE Human secreted/transmembrane protein, PRO4993.
PN US2003054986-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 45.1%; Score 815; DB 7; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.6e-61;

Best Local Similarity 47.5%; Pred. No. 1.6e-61;
RESULT 568
ID ADC62020 standard; protein; 352 AA.
DE Human secreted/transmembrane protein, PRO4993.
PN US2003049684-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 45.1%; Score 815; DB 7; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.6e-61;
RESULT 569
ID ADC63984 standard; protein; 352 AA.
DE Human secreted/transmembrane protein, PRO4993.
PN US2003054405-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 45.1%; Score 815; DB 7; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.6e-61;
RESULT 570
ID ADC67084 standard; protein; 352 AA.
DE Human secreted/transmembrane protein, PRO4993.
PN US2003060406-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 45.1%; Score 815; DB 7; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.6e-61;
RESULT 571
ID ADC69208 standard; protein; 352 AA.
DE Human secreted/transmembrane protein, PRO4993.
PN US2003064407-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 45.1%; Score 815; DB 7; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.6e-61;
RESULT 572
ID ADC63268 standard; protein; 352 AA.
DE Human secreted/transmembrane protein, PRO4993.
PN US2003068648-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 45.1%; Score 815; DB 7; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.6e-61;
RESULT 573
ID ADC68333 standard; protein; 352 AA.
DE Human secreted/transmembrane protein, PRO4993.
PN US2003069178-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 45.1%; Score 815; DB 7; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.6e-61;
RESULT 574
ID ADC41653 standard; protein; 352 AA.
DE Human secreted/transmembrane protein, PRO4993.
PN US2003072745-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 45.1%; Score 815; DB 7; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.6e-61;
RESULT 575
ID ADC67708 standard; protein; 352 AA.
DE Human secreted/transmembrane protein, PRO4993.
PN US2003073131-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 45.1%; Score 815; DB 7; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.6e-61;
RESULT 576
ID ADC62644 standard; protein; 352 AA.
DE Human secreted/transmembrane protein, PRO4993.
PN US2003073624-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 45.1%; Score 815; DB 7; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.6e-61;
RESULT 577
ID ADC42277 standard; protein; 352 AA.
DE Human secreted/transmembrane protein, PRO4993.
PN US2003104998-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 45.1%; Score 815; DB 7; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.6e-61;
RESULT 578
ID ADE49646 standard; protein; 352 AA.
DE Human secreted/transmembrane protein, PRO4993.
PN US2003096744-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.1%; Score 815; DB 7; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.6e-61;
RESULT 579
ID ADE35700 standard; protein; 352 AA.
DE Human secreted/transmembrane protein, PRO4993.
PN US2003203434-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.1%; Score 815; DB 7; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.6e-61;
RESULT 580
ID ADE16814 standard; protein; 352 AA.
DE Human secreted/transmembrane protein, PRO4993.
PN US2003203435-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.1%; Score 815; DB 7; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.6e-61;
RESULT 581
ID ADD73429 standard; protein; 352 AA.
DE Human secreted/transmembrane protein, PRO4993.
PN US2003203436-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.1%; Score 815; DB 7; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.6e-61;
RESULT 582
ID ADD72787 standard; protein; 352 AA.
DE Human secreted/transmembrane protein, PRO4993.
PN US2003194781-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.1%; Score 815; DB 7; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.6e-61;
RESULT 583
ID ADE17438 standard; protein; 352 AA.
DE Human secreted/transmembrane protein, PRO4993.
PN US2003203433-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.1%; Score 815; DB 7; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.6e-61;
RESULT 584
ID ADF47452 standard; protein; 352 AA.
DE Human secreted/transmembrane protein, PRO4993.
PN US2003195333-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.1%; Score 815; DB 7; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.6e-61;
RESULT 585
ID ADG53209 standard; protein; 352 AA.
DE Human secreted/transmembrane protein, PRO4993.
PN US2003216561-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.1%; Score 815; DB 7; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.6e-61;
RESULT 586
ID ADG53209 standard; protein; 352 AA.
DE Human secreted/transmembrane protein, PRO4993.
PN US2003216561-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.1%; Score 815; DB 7; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.6e-61;

ID ADG60529 standard; protein; 352 AA.
DE Human secreted/transmembrane protein, PRO4993.
PN US2003206915-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.1%; Score 815; DB 7; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.6e-61;
RESULT 587
ID ADI61289 standard; protein; 352 AA.
DE Human secreted/transmembrane protein, PRO4993.
PN US2003077700-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 45.1%; Score 815; DB 7; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.6e-61;
RESULT 588
ID ADE48946 standard; protein; 352 AA.
DE Human secreted/transmembrane protein, PRO4993.
PN US2003104536-A1.
PD 03-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 45.1%; Score 815; DB 8; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.6e-61;
RESULT 589
ID ADE90047 standard; protein; 352 AA.
DE Human secreted/transmembrane protein, PRO4993.
PN US2003130181-A1.
PD 10-JUL-2003.
PA (ASHK/) ASHKENAZI A J.
PA (BAKE/) BAKER K P.
PA (BOTS/) BOTSTEIN D.
PA (DESN/) DESNOYERS L.
PA (EATO/) EATON D L.
PA (FERR/) FERRARA N.
PA (FILV/) FILVAROFF E.
PA (FONG/) FONG S.
PA (GROW/) GAO W.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GIRM/) GIRMALDI J C.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (KLJA/) KLJAVIN I J.
PA (KUOS/) KUO S S.
PA (NAPI/) NAPIER M A.
PA (PANJ/) PAN J.
PA (PAON/) PAONI N F.
PA (ROYM/) ROY M A.
PA (SHEL/) SHELTON D L.
PA (STEW/) STEWART T A.
PA (TUMA/) TUMAS D.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 45.1%; Score 815; DB 8; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.6e-61;
RESULT 590
ID ADF61687 standard; protein; 352 AA.
DE Human secreted/transmembrane protein, PRO4993.
PN US2003195345-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.1%; Score 815; DB 8; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.6e-61;
RESULT 591
ID ADF40379 standard; protein; 352 AA.
DE Human secreted/transmembrane protein, PRO4993.
PN US2003198994-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.1%; Score 815; DB 8; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.6e-61;
RESULT 592
ID ADF46175 standard; protein; 352 AA.
DE Human secreted/transmembrane protein, PRO4993.
PN US2003195148-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.1%; Score 815; DB 8; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.6e-61;
RESULT 593
ID ADF24571 standard; protein; 352 AA.
DE Human secreted/transmembrane protein, PRO4993.
PN US2003204055-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.1%; Score 815; DB 8; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.6e-61;
RESULT 594
ID ADF41003 standard; protein; 352 AA.
DE Human secreted/transmembrane protein, PRO4993.
PN US2003199021-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.1%; Score 815; DB 8; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.6e-61;
RESULT 595
ID ADF23947 standard; protein; 352 AA.
DE Human secreted/transmembrane protein, PRO4993.
PN US2003203402-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.1%; Score 815; DB 8; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.6e-61;
RESULT 596
ID ADF33930 standard; protein; 352 AA.
DE Human secreted/transmembrane protein, PRO4993.
PN US2003194780-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.1%; Score 815; DB 8; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.6e-61;
RESULT 597
ID ADF27397 standard; protein; 352 AA.
DE Human secreted/transmembrane protein, PRO4993.
PN US2003199436-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.1%; Score 815; DB 8; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.6e-61;
RESULT 598
ID ADF28033 standard; protein; 352 AA.
DE Human secreted/transmembrane protein, PRO4993.
PN US2003199437-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.1%; Score 815; DB 8; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.6e-61;
RESULT 599
ID ADF41627 standard; protein; 352 AA.
DE Human secreted/transmembrane protein, PRO4993.
PN US2003199435-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.1%; Score 815; DB 8; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.6e-61;
RESULT 600
ID ADF33306 standard; protein; 352 AA.
DE Human secreted/transmembrane protein, PRO4993.
PN US2003211091-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.1%; Score 815; DB 8; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.6e-61;
RESULT 601
ID ADF33306 standard; protein; 352 AA.
DE Human secreted/transmembrane protein, PRO4993.
PN US2003211091-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.1%; Score 815; DB 8; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.6e-61;

ID ADF25672 standard; protein; 352 AA.
DE Human secreted/transmembrane protein, PRO4993.
PN US2003211092-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.1%; Score 815; DB 8; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.6e-61;
RESULT 602
ID ADF26773 standard; protein; 352 AA.
DE Human secreted/transmembrane protein, PRO4993.
PN US2003199674-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.1%; Score 815; DB 8; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.6e-61;
RESULT 603
ID ADF34562 standard; protein; 352 AA.
DE Human secreted/transmembrane protein, PRO4993.
PN US2003194410-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.1%; Score 815; DB 8; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.6e-61;
RESULT 604
ID ADF46799 standard; protein; 352 AA.
DE Human secreted/transmembrane protein, PRO4993.
PN US2003195344-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.1%; Score 815; DB 8; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.6e-61;
RESULT 605
ID ADG50785 standard; protein; 352 AA.
DE Human secreted/transmembrane protein, PRO4993.
PN US2003207803-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.1%; Score 815; DB 8; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.6e-61;
RESULT 606
ID ADG50161 standard; protein; 352 AA.
DE Human secreted/transmembrane protein, PRO4993.
PN US2003215905-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.1%; Score 815; DB 8; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.6e-61;
RESULT 607
ID ADG52033 standard; protein; 352 AA.
DE Human secreted/transmembrane protein, PRO4993.
PN US2003215908-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.1%; Score 815; DB 8; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.6e-61;
RESULT 608
ID ADG49537 standard; protein; 352 AA.
DE Human secreted/transmembrane protein, PRO4993.
PN US2003216305-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.1%; Score 815; DB 8; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.6e-61;
RESULT 609
ID ADG48913 standard; protein; 352 AA.
DE Human secreted/transmembrane protein, PRO4993.
PN US2003216560-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.1%; Score 815; DB 8; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.6e-61;
RESULT 610
ID ADG51409 standard; protein; 352 AA.

DE Human secreted/transmembrane protein, PRO4993.
PN US2004005312-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 45.1%; Score 815; DB 8; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.6e-61;
RESULT 611
ID ADG59353 standard; protein; 352 AA.
DE Human secreted/transmembrane protein, PRO4993.
PN US2004005657-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 45.1%; Score 815; DB 8; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.6e-61;
RESULT 612
ID ADG62809 standard; protein; 352 AA.
DE Human secreted/transmembrane protein, PRO4993.
PN US2004006219-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 45.1%; Score 815; DB 8; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.6e-61;
RESULT 613
ID ADM17611 standard; protein; 352 AA.
DE Human secreted/transmembrane protein, PRO4993.
PN US2004048332-A1.
PD 11-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 45.1%; Score 815; DB 8; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.6e-61;
RESULT 614
ID ADL07445 standard; protein; 352 AA.
DE Human secreted/transmembrane protein, PRO4993.
PN US2004063921-A1.
PD 01-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 45.1%; Score 815; DB 8; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.6e-61;
RESULT 615
ID ADU50567 standard; protein; 352 AA.
DE PRO4993, SEQ ID 612.
PN US2004223964-A1.
PD 11-NOV-2004.
PA (GETH) GENENTECH INC.
Query Match 45.1%; Score 815; DB 8; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.6e-61;
RESULT 616
ID ADM49846 standard; protein; 352 AA.
DE PRO4993 protein, SEQ ID 612.
PN US2005014226-A1.
PD 20-JAN-2005.
PA (ASHK/) ASHKENAZI A J.
PA (BAKE/) BAKER K P.
PA (BOTS/) BOTSTEIN D.
PA (DESN/) DESNOYERS L.
PA (EATO/) EATON D L.
PA (FERR/) FERRARA N.
PA (FILV/) FILVAROFF E.
PA (FONG/) FONG S.
PA (GAOW/) GAO W.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GRIM/) GRIMALDI J C.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (KLJA/) KLJAVIN I J.
PA (KOOS/) KOO S S.
PA (NAPI/) NAPIER M A.
PA (PANJ/) PAN J.
PA (PAON/) PAONI N F.
PA (ROYM/) ROY M A.

PA (SHEL/) SHELTON D L.
PA (STEW/) STEWART T A.
PA (TUMA/) TUMAS D.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 45.1%; Score 815; DB 9; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.6e-61;
RESULT 617
ID ADZ52507 standard; protein; 352 AA.
DE Human secreted/transmembrane protein, PRO4993.
PN US2005084935-A1.
PD 21-APR-2005.
PA (ASHK/) ASHKENAZI A J.
PA (BAKE/) BAKER K P.
PA (BOTS/) BOTSTEIN D.
PA (DESN/) DESNOYERS L.
PA (SATO/) EATON D L.
PA (FERR/) FERRARA N.
PA (FILV/) FILVAROFF E.
PA (FONG/) FONG S.
PA (GAOW/) GAO W.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GRIM/) GRIMALDI J C.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (KLJA/) KLJAVIN I J.
PA (KUOS/) KUO S S.
PA (NAPI/) NAPIER M A.
PA (PANG/) PAN J.
PA (PAON/) PAONI N F.
PA (ROYM/) ROY M A.
PA (SHEL/) SHELTON D L.
PA (STEW/) STEWART T A.
PA (TUMA/) TUMAS D.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 45.1%; Score 815; DB 9; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.6e-61;
RESULT 618
ID AED48335 standard; protein; 352 AA.
DE Human PRO4993 amino acid sequence.
PN US2005227342-A1.
PD 13-OCT-2005.
PA (GETH/) GENENTECH INC.
Query Match 45.1%; Score 815; DB 9; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.6e-61;
RESULT 619
ID AAW05167 standard; protein; 252 AA.
DE Human LAMP residues 46-294.
PN WO9630052-A1.
PD 03-OCT-1996.
PA (UMDN-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.
Query Match 44.1%; Score 796.5; DB 2; Length 252;
Best Local Similarity 56.9%; Pred. No. 4.1e-60;
RESULT 620
ID AAW05168 standard; protein; 252 AA.
DE Rat LAMP residues 46-294.
PN WO9630052-A1.
PD 03-OCT-1996.
PA (UMDN-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.
Query Match 44.0%; Score 795.5; DB 2; Length 252;
Best Local Similarity 56.9%; Pred. No. 5e-60;
RESULT 621
ID ABG96271 standard; protein; 336 AA.
DE Human immunoglobulin superfamily protein IGSFP-9.
PN WO200272794-A2.
PD 19-SEP-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 42.2%; Score 763; DB 5; Length 336;
Best Local Similarity 50.6%; Pred. No. 4.7e-57;
RESULT 622
ID AAE29924 standard; protein; 336 AA.
DE Human LP289 protein.
PN WO200274906-A2.
PD 26-SEP-2002.
PA (ELIL) LILLY & CO ELI.
Query Match 42.2%; Score 763; DB 6; Length 336;
Best Local Similarity 50.6%; Pred. No. 4.7e-57;
RESULT 623
ID ADH71418 standard; protein; 336 AA.
DE Human protein of the invention NOV11q SEQ ID NO:314.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 42.2%; Score 763; DB 8; Length 336;
Best Local Similarity 50.6%; Pred. No. 4.7e-57;
RESULT 624
ID ADH71412 standard; protein; 336 AA.
DE Human protein of the invention NOV1ln SEQ ID NO:308.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 42.2%; Score 763; DB 8; Length 336;
Best Local Similarity 50.6%; Pred. No. 4.7e-57;
RESULT 625
ID ADH71414 standard; protein; 336 AA.
DE Human protein of the invention NOV1lb SEQ ID NO:284.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 42.2%; Score 763; DB 8; Length 336;
Best Local Similarity 50.6%; Pred. No. 4.7e-57;
RESULT 626
ID ADH71388 standard; protein; 344 AA.
DE Human protein of the invention NOV11b SEQ ID NO:284.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 42.2%; Score 763; DB 8; Length 344;
Best Local Similarity 50.6%; Pred. No. 4.8e-57;
RESULT 627
ID ADH71390 standard; protein; 325 AA.
DE Human protein of the invention NOV11c SEQ ID NO:286.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 42.2%; Score 762; DB 8; Length 325;
Best Local Similarity 50.5%; Pred. No. 5.5e-57;
RESULT 628
ID AAE30252 standard; protein; 306 AA.
DE Human LP289 mature protein #1.
PN WO200274906-A2.
PD 26-SEP-2002.
PA (ELIL) LILLY & CO ELI.
Query Match 42.1%; Score 761; DB 6; Length 306;
Best Local Similarity 52.5%; Pred. No. 6.1e-57;
RESULT 629
ID ADH71402 standard; protein; 307 AA.
DE Human protein of the invention NOV11i SEQ ID NO:298.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 42.1%; Score 761; DB 8; Length 307;
Best Local Similarity 52.5%; Pred. No. 6.2e-57;
RESULT 630
ID ADH71410 standard; protein; 309 AA.
DE Human protein of the invention NOV1lm SEQ ID NO:306.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 42.1%; Score 761; DB 8; Length 309;
Best Local Similarity 52.5%; Pred. No. 6.2e-57;
RESULT 631

ID ADH71406 standard; protein; 309 AA.
DE Human protein of the invention NOV11k SEQ ID NO:302.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 42.1%; Score 761; DB 8; Length 309;
Best Local Similarity 52.5%; Pred. No. 6.2e-57;
RESULT 632
ID AAE30253 standard; protein; 314 AA.
DE Human LP289 mature protein #2.
PN WO200274906-A2.
PD 26-SEP-2002.
PA (LIL) LILLY & CO ELI.
Query Match 42.1%; Score 761; DB 6; Length 314;
Best Local Similarity 52.5%; Pred. No. 6.4e-57;
RESULT 633
ID ADH71394 standard; protein; 315 AA.
DE Human protein of the invention NOV1e SEQ ID NO:290.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 42.1%; Score 761; DB 8; Length 315;
Best Local Similarity 52.5%; Pred. No. 6.4e-57;
RESULT 634
ID ABG94637 standard; protein; 319 AA.
DE Human NOV5b protein.
PN WO200266643-A2.
PD 29-AUG-2002.
PA (CURA-) CURAGEN CORP.
Query Match 42.1%; Score 761; DB 5; Length 319;
Best Local Similarity 52.5%; Pred. No. 6.5e-57;
RESULT 635
ID ABG94636 standard; protein; 319 AA.
DE Human NOV5a protein.
PN WO200266643-A2.
PD 29-AUG-2002.
PA (CURA-) CURAGEN CORP.
Query Match 42.1%; Score 761; DB 5; Length 319;
Best Local Similarity 52.5%; Pred. No. 6.5e-57;
RESULT 636
ID ADL35977 standard; protein; 319 AA.
DE Human NOVX polypeptide #11.
PN US2003207800-A1.
PD 06-NOV-2003.
PA (MALY/) MALYANKAR U M.
PA (SHEN/) SHENOY S G.
PA (SPYT/) SPYTEK K A.
PA (ZERH/) ZERHUSEN B D.
PA (PATT/) PATTURAJAN M.
PA (GUOX/) GUO X.
PA (KEKU/) KEKUDA R.
PA (GANG/) GANGOLLI E A.
PA (SHIM/) SHIMKETS R A.
PA (TAUP/) TAUPIER R J.
PA (LIL/) LI L.
PA (PADI/) PADIGARU M.
Query Match 42.1%; Score 761; DB 7; Length 319;
Best Local Similarity 52.5%; Pred. No. 6.5e-57;
RESULT 637
ID ADL35979 standard; protein; 319 AA.
DE Human NOVX polypeptide #12.
PN US2003207800-A1.
PD 06-NOV-2003.
PA (MALY/) MALYANKAR U M.
PA (SHEN/) SHENOY S G.
PA (SPYT/) SPYTEK K A.
PA (ZERH/) ZERHUSEN B D.
PA (PATT/) PATTURAJAN M.
PA (GUOX/) GUO X.
PA (KEKU/) KEKUDA R.
PA (GANG/) GANGOLLI E A.
PA (SHIM/) SHIMKETS R A.
PA (TAUP/) TAUPIER R J.

PA (LIL/) LI L.
PA (PADI/) PADIGARU M.
Query Match 42.1%; Score 761; DB 7; Length 319;
Best Local Similarity 52.5%; Pred. No. 6.5e-57;
RESULT 638
ID ADH71400 standard; protein; 319 AA.
DE Human protein of the invention NOV11h SEQ ID NO:296.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 42.1%; Score 761; DB 8; Length 319;
Best Local Similarity 52.5%; Pred. No. 6.5e-57;
RESULT 639
ID ADH71396 standard; protein; 319 AA.
DE Human protein of the invention NOV11f SEQ ID NO:292.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 42.1%; Score 761; DB 8; Length 319;
Best Local Similarity 52.5%; Pred. No. 6.5e-57;
RESULT 640
ID ADH71416 standard; protein; 320 AA.
DE Human protein of the invention NOV11p SEQ ID NO:312.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 42.1%; Score 761; DB 8; Length 320;
Best Local Similarity 52.5%; Pred. No. 6.5e-57;
RESULT 641
ID ADH71398 standard; protein; 325 AA.
DE Human protein of the invention NOV11g SEQ ID NO:294.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 42.1%; Score 761; DB 8; Length 325;
Best Local Similarity 52.5%; Pred. No. 6.7e-57;
RESULT 642
ID ADH71422 standard; protein; 336 AA.
DE Human protein of the invention NOV11s SEQ ID NO:318.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 42.1%; Score 760; DB 8; Length 336;
Best Local Similarity 50.6%; Pred. No. 8.5e-57;
RESULT 643
ID ADH71386 standard; protein; 336 AA.
DE Human protein of the invention NOV11a SEQ ID NO:282.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 42.1%; Score 760; DB 8; Length 336;
Best Local Similarity 50.6%; Pred. No. 8.5e-57;
RESULT 644
ID ABG94638 standard; protein; 307 AA.
DE Human NOV5c protein.
PN WO200266643-A2.
PD 29-AUG-2002.
PA (CURA-) CURAGEN CORP.
Query Match 41.9%; Score 757; DB 5; Length 307;
Best Local Similarity 52.5%; Pred. No. 1.4e-56;
RESULT 645
ID ADH71404 standard; protein; 319 AA.
DE Human protein of the invention NOV11j SEQ ID NO:300.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 41.9%; Score 757; DB 8; Length 319;
Best Local Similarity 52.5%; Pred. No. 1.4e-56;
RESULT 646
ID ADH71420 standard; protein; 336 AA.
DE Human protein of the invention NOV11r SEQ ID NO:316.
PN WO2003102155-A2.
PD 11-DEC-2003.

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PA (CURA-) CURAGEN CORP.
Query Match 41.9%; Score 757; DB 8; Length 336;
Best Local Similarity 50.3%; Pred. No. 1.5e-56;
RESULT 647
ID ADP29916 standard; protein; 278 AA.
DE Human secreted protein SEQ ID #1914.
PN WO2004035732-A2.
PD 29-APR-2004.
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
Query Match 41.7%; Score 752.5; DB 8; Length 278;
Best Local Similarity 54.1%; Pred. No. 2.9e-56;
RESULT 648
ID AAE30254 standard; protein; 284 AA.
DE Human LP289 mature protein #3.
PN WO200274906-A2.
PD 26-SEP-2002.
PA (ELIL ) LILLY & CO ELI.
Query Match 41.7%; Score 752.5; DB 6; Length 284;
Best Local Similarity 54.1%; Pred. No. 3e-56;
RESULT 649
ID AAE30256 standard; protein; 291 AA.
DE Human LP289 mature protein #5.
PN WO200274906-A2.
PD 26-SEP-2002.
PA (ELIL ) LILLY & CO ELI.
Query Match 41.7%; Score 752.5; DB 6; Length 291;
Best Local Similarity 54.1%; Pred. No. 3.1e-56;
RESULT 650
ID AAE30255 standard; protein; 292 AA.
DE Human LP289 mature protein #4.
PN WO200274906-A2.
PD 26-SEP-2002.
PA (ELIL ) LILLY & CO ELI.
Query Match 41.7%; Score 752.5; DB 6; Length 292;
Best Local Similarity 54.1%; Pred. No. 3.1e-56;
RESULT 651
ID ADL35981 standard; protein; 305 AA.
DE Human NOVX polypeptide #13.
PN US2003207800-A1.
PD 06-NOV-2003.
PA (MALY/) MALYANKAR U M.
PA (SHEN/) SHENOY S G.
PA (SPYT/) SPYTEK K A.
PA (ZERH/) ZERHUSEN B D.
PA (PATT/) PATTURAJAN M.
PA (GUOX/) GUO X.
PA (KEKU/) KEKUDA R.
PA (GANG/) GANGOLLI E A.
PA (SHIM/) SHIMKETS R A.
PA (TAUP/) TAUPIER R J.
PA (LILL/) LI L.
PA (PADI/) PADIGARU M.
Query Match 40.3%; Score 727; DB 7; Length 305;
Best Local Similarity 51.8%; Pred. No. 5.2e-54;
RESULT 652
ID AAU84386 standard; protein; 336 AA.
DE Novel human secreted or membrane-associated protein #25.
PN WO200204600-A2.
PD 17-JAN-2002.
PA (SMIK ) SMITHKLINE BEECHAM CORP.
PA (SMIK ) SMITHKLINE BEECHAM PLC.
PA (GLAX ) GLAXO GROUP LTD.
Query Match 40.2%; Score 726; DB 5; Length 336;
Best Local Similarity 50.5%; Pred. No. 7.3e-54;
RESULT 653
ID ABG94639 standard; protein; 336 AA.
DE Human NOV5d protein.
PN WO200266643-A2.
PD 29-AUG-2002.
PA (CURA-) CURAGEN CORP.
Query Match 39.9%; Score 721; DB 5; Length 336;
Best Local Similarity 50.5%; Pred. No. 2e-53;
RESULT 654
PA (CURA-) CURAGEN CORP.
Query Match 39.9%; Score 721; DB 8; Length 336;
Best Local Similarity 50.5%; Pred. No. 2e-53;
RESULT 655
ID ABB10253 standard; protein; 281 AA.
DE Human CDNA SEQ ID NO: 561.
PN WO200154474-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 39.9%; Score 720.5; DB 4; Length 281;
Best Local Similarity 50.4%; Pred. No. 1.7e-53;
RESULT 656
ID ABP66840 standard; protein; 281 AA.
DE Human polypeptide SEQ ID NO 561.
PN US2002030672-A1.
PD 11-JUL-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 39.9%; Score 720.5; DB 5; Length 281;
Best Local Similarity 50.4%; Pred. No. 1.7e-53;
RESULT 657
ID ADL35983 standard; protein; 336 AA.
DE Human NOVX polypeptide #14.
PN US2003207800-A1.
PD 06-NOV-2003.
PA (MALY/) MALYANKAR U M.
PA (SHEN/) SHENOY S G.
PA (SPYT/) SPYTEK K A.
PA (ZERH/) ZERHUSEN B D.
PA (PATT/) PATTURAJAN M.
PA (GUOX/) GUO X.
PA (KEKU/) KEKUDA R.
PA (GANG/) GANGOLLI E A.
PA (SHIM/) SHIMKETS R A.
PA (TAUP/) TAUPIER R J.
PA (LILL/) LI L.
PA (PADI/) PADIGARU M.
Query Match 39.4%; Score 712; DB 7; Length 336;
Best Local Similarity 50.2%; Pred. No. 1.2e-52;
RESULT 658
ID ADH71392 standard; protein; 253 AA.
DE Human protein of the invention NOV11d SEQ ID NO:288.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 38.1%; Score 687.5; DB 8; Length 253;
Best Local Similarity 55.6%; Pred. No. 1e-50;
RESULT 659
ID AAU84385 standard; protein; 351 AA.
DE Novel human secreted or membrane-associated protein #24.
PN WO200204600-A2.
PD 17-JAN-2002.
PA (SMIK ) SMITHKLINE BEECHAM CORP.
PA (SMIK ) SMITHKLINE BEECHAM PLC.
PA (GLAX ) GLAXO GROUP LTD.
Query Match 37.7%; Score 681.5; DB 5; Length 351;
Best Local Similarity 50.7%; Pred. No. 5.3e-50;
RESULT 660
ID ABG13848 standard; protein; 141 AA.
DE Novel human diagnostic protein #13839.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 33.4%; Score 603; DB 4; Length 141;
Best Local Similarity 86.6%; Pred. No. 9e-44;
RESULT 661
ID AAE30271 standard; protein; 294 AA.
DE Human LP319b protein variant #2.
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PN WO200274906-A2.
PD 26-SEP-2002.
PA (ELIL) LILLY & CO ELI.
Query Match 33.4%; Score 603; DB 6; Length 294;
Best Local Similarity 45.0%; Pred. No. 2.5e-43;
RESULT 662
ID AAE30270 standard; protein; 286 AA.
DE Human LP319b protein variant #1.
PN WO200274906-A2.
PD 26-SEP-2002.
PA (ELIL) LILLY & CO ELI.
Query Match 33.2%; Score 600; DB 6; Length 286;
Best Local Similarity 45.0%; Pred. No. 4.3e-43;
RESULT 663
ID ADP29917 standard; protein; 222 AA.
DE Human secreted protein SEQ ID #1915.
PN WO2004035732-A2.
PD 29-APR-2004.
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
Query Match 33.2%; Score 599.5; DB 8; Length 222;
Best Local Similarity 54.0%; Pred. No. 3.4e-43;
RESULT 664
ID ABG13847 standard; protein; 130 AA.
DE Novel human diagnostic protein #13838.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 31.5%; Score 569.5; DB 4; Length 130;
Best Local Similarity 88.9%; Pred. No. 6.3e-41;
RESULT 665
ID AAE30269 standard; protein; 234 AA.
DE Human LP319b protein mature sequence #2.
PN WO200274906-A2.
PD 26-SEP-2002.
PA (ELIL) LILLY & CO ELI.
Query Match 29.2%; Score 527; DB 6; Length 234;
Best Local Similarity 53.2%; Pred. No. 6.5e-37;
RESULT 666
ID AAE29927 standard; protein; 256 AA.
DE Human LP319b protein.
PN WO200274906-A2.
PD 26-SEP-2002.
PA (ELIL) LILLY & CO ELI.
Query Match 29.2%; Score 527; DB 6; Length 256;
Best Local Similarity 53.2%; Pred. No. 7.3e-37;
RESULT 667
ID ABG13816 standard; protein; 872 AA.
DE Novel human diagnostic protein #13807.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 29.1%; Score 525.5; DB 4; Length 872;
Best Local Similarity 43.4%; Pred. No. 5.3e-36;
RESULT 668
ID AD508994 standard; protein; 872 AA.
DE Novel protein-related contig polypeptide sequence #60.
PN WO2003054152-A2.
PD 03-JUL-2003.
PA (HYSE-) HYSEQ INC.
Query Match 29.1%; Score 525.5; DB 7; Length 872;
Best Local Similarity 43.4%; Pred. No. 5.3e-36;
RESULT 669
ID AAE30268 standard; protein; 226 AA.
DE Human LP319b protein mature sequence #1.
PN WO200274906-A2.
PD 26-SEP-2002.
PA (ELIL) LILLY & CO ELI.
Query Match 28.0%; Score 505; DB 6; Length 226;
Best Local Similarity 53.0%; Pred. No. 4.9e-35;
RESULT 670
ID AAE30264 standard; protein; 211 AA.
DE Human LP319a protein mature sequence #1.
PN WO200274906-A2.

PD 26-SEP-2002.
PA (ELIL) LILLY & CO ELI.
Query Match 26.1%; Score 472; DB 6; Length 211;
Best Local Similarity 54.1%; Pred. No. 3.1e-32;
RESULT 671
ID AAE30265 standard; protein; 222 AA.
DE Human LP319a protein mature sequence #2.
PN WO200274906-A2.
PD 26-SEP-2002.
PA (ELIL) LILLY & CO ELI.
Query Match 26.1%; Score 472; DB 6; Length 222;
Best Local Similarity 54.1%; Pred. No. 3.4e-32;
RESULT 672
ID AAE29926 standard; protein; 241 AA.
DE Human LP319a protein.
PN WO200274906-A2.
PD 26-SEP-2002.
PA (ELIL) LILLY & CO ELI.
Query Match 26.1%; Score 472; DB 6; Length 241;
Best Local Similarity 54.1%; Pred. No. 3.7e-32;
RESULT 673
ID ABB69485 standard; protein; 413 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 35247.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 18.7%; Score 338.5; DB 4; Length 413;
Best Local Similarity 28.0%; Pred. No. 2.6e-20;
RESULT 674
ID ABB65642 standard; protein; 315 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 23718.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 18.4%; Score 333; DB 4; Length 315;
Best Local Similarity 31.9%; Pred. No. 5.3e-20;
RESULT 675
ID ABB62574 standard; protein; 545 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 14514.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 16.9%; Score 306; DB 4; Length 545;
Best Local Similarity 28.9%; Pred. No. 2.4e-17;
RESULT 676
ID ABB58947 standard; protein; 333 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 3633.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 16.5%; Score 297.5; DB 4; Length 333;
Best Local Similarity 29.7%; Pred. No. 6.6e-17;
RESULT 677
ID ADS10483 standard; protein; 2537 AA.
DE Human therapeutic protein - SEQ ID 720.
PN WO2004080148-A2.
PD 23-SEP-2004.
PA (NUVE-) NUVELO INC.
Query Match 16.1%; Score 290.5; DB 8; Length 2537;
Best Local Similarity 29.8%; Pred. No. 4.2e-15;
RESULT 678
ID ADS98860 standard; protein; 2537 AA.
DE Protein factor discovery related human contig polypeptide, SEQ ID 1124.
PN WO2004087874-A2.
PD 14-OCT-2004.
PA (NUVE-) NUVELO INC.
PA (DRMA/) DRMANAC R T.
Query Match 16.1%; Score 290.5; DB 8; Length 2537;
Best Local Similarity 29.8%; Pred. No. 4.2e-15;
RESULT 679
ID ABU12083 standard; protein; 2572 AA.
DE Human NOV25b CG93858-02 protein SEQ ID 86.
PN WO200281625-A2.

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PD 17-OCT-2002.
PA (CURA-) CURAGEN CORP.
Query Match 16.1%; Score 290.5; DB 6; Length 2572;
Best Local Similarity 29.8%; Pred. No. 4.3e-15;
RESULT 680
ID ADK60225 standard; protein; 2673 AA.
DE Angiogenesis differentially expressed protein GS-P52.
PN FR2836687-A1.
PD 05-SEP-2003.
PA (GENE-) GENE SIGNAL.
PA (ALMA/) AL MAHMOOD S.
Query Match 16.1%; Score 290.5; DB 8; Length 2673;
Best Local Similarity 29.8%; Pred. No. 4.6e-15;
RESULT 681
ID ADK60526 standard; protein; 2673 AA.
DE Angiogenesis differentially expressed protein GS-P52.
PN FR2836686-A1.
PD 05-SEP-2003.
PA (GENE-) GENE SIGNAL.
PA (ALMA/) AL MAHMOOD S.
Query Match 16.1%; Score 290.5; DB 8; Length 2673;
Best Local Similarity 29.8%; Pred. No. 4.6e-15;
RESULT 682
ID ADP73149 standard; protein; 2673 AA.
DE Angiogenesis inhibitor human protein sequence, GS-P52.
PN FR2843753-A1.
PD 27-FEB-2004.
PA (GENE-) GENE S.
PA (ALMS/) AL M S.
Query Match 16.1%; Score 290.5; DB 8; Length 2673;
Best Local Similarity 29.8%; Pred. No. 4.6e-15;
RESULT 683
ID ABU69135 standard; protein; 4495 AA.
DE Human NOVX polypeptide #10.
PN WO200290504-A2.
PD 14-NOV-2002.
PA (CURA-) CURAGEN CORP.
Query Match 16.1%; Score 290.5; DB 6; Length 4495;
Best Local Similarity 29.8%; Pred. No. 9.3e-15;
RESULT 684
ID ADH72106 standard; protein; 4495 AA.
DE Human protein of the invention NOV43c SEQ ID NO:1002.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 16.1%; Score 290.5; DB 8; Length 4495;
Best Local Similarity 29.8%; Pred. No. 9.3e-15;
RESULT 685
ID ADO08273 standard; protein; 4495 AA.
DE Human NOVX polypeptide #10.
PN US2004018594-A1.
PD 29-JAN-2004.
PA (ALSO/) ALSOBROOK J P.
PA (ANDE/) ANDERSON D W.
PA (BOLD/) BOLDOG F L.
PA (BURG/) BURGESS C E.
PA (CASM/) CASHMAN S J.
PA (CHAP/) CHAPOVAL A.
PA (EDIN/) EDINGER S R.
PA (GERL/) GERLACH V.
PA (GORM/) GORMAN L.
PA (GUNT/) GUNTHER E.
PA (GUOX/) GUO X S.
PA (KEKU/) KEKUDA R.
PA (LEPL/) LEPLEY D M.
PA (LILL/) LI L.
PA (LIUX/) LIU X.
PA (MALY/) MALYANKAR U M.
PA (MILL/) MILLER C E.
PA (MILL/) MILLET I.
PA (PADI/) PADIGARU M.
PA (PATT/) PATTURAJAN M.
PA (PENA/) PENA C E A.
PA (RIEG/) RIEGER D K.
PA (SHEN/) SHENOV S G.
PA (SHIM/) SHIMKETS R A.
PA (SPYT/) SPYTEK K A.
PA (TAUF/) TAUPIER R J.
PA (VERN/) VERNET C A M.
PA (VOSS/) VOSS E Z.
PA (ZERH/) ZERHUSEN B D.
Query Match 16.1%; Score 290.5; DB 8; Length 4495;
Best Local Similarity 29.8%; Pred. No. 9.3e-15;
RESULT 686
ID ADJ70089 standard; protein; 5636 AA.
DE Human heat mitochondrial protein as a therapeutic target SeqID1895.
PN WO2003087768-A2.
PD 23-OCT-2003.
PA (MITO-) MITOKOR.
PA (BUCK-) BUCK INST AGE RES.
Query Match 16.1%; Score 290.5; DB 7; Length 5636;
Best Local Similarity 31.1%; Pred. No. 1.3e-14;
RESULT 687
ID ADJ8137 standard; protein; 5636 AA.
DE Human hemocentin protein - SEQ ID 128.
PN US2003170630-A1.
PD 11-SEP-2003.
PA (ALSO/) ALSOBROOK J P.
PA (TCHE/) TCHERNEV V T.
PA (LIUX/) LIU X.
PA (SPYT/) SPYTEK K A.
PA (ZERH/) ZERHUSEN B D.
PA (PATT/) PATTURAJAN M.
PA (LEPL/) LEPLEY D M.
PA (BURG/) BURGESS C E.
PA (SHIM/) SHIMKETS R A.
PA (GROS/) GROSSE W M.
PA (SZEK/) SZEKERES E S.
PA (VERN/) VERNET C A M.
PA (LILL/) LI L.
PA (CASM/) CASHMAN S J.
PA (BOLD/) BOLDOG F L.
PA (GORM/) GORMAN L.
PA (GANG/) GANGOLLI E A.
PA (FERN/) FERNANDES E R.
PA (RIEG/) RIEGER D K.
PA (EDIN/) EDINGER S R.
PA (GUNT/) GUNTHER E.
PA (MILL/) MILLET I.
PA (SCIO/) SCIORE P.
PA (ELLE/) ELLERMAN K.
PA (MACD/) MACDOUGALL J R.
PA (SMIT/) SMITHSON G.
Query Match 16.1%; Score 290.5; DB 7; Length 5636;
Best Local Similarity 31.1%; Pred. No. 1.3e-14;
RESULT 688
ID ADK60205 standard; protein; 5636 AA.
DE Angiogenesis differentially expressed protein GS-P29.
PN FR2836687-A1.
PD 05-SEP-2003.
PA (GENE-) GENE SIGNAL.
PA (ALMA/) AL MAHMOOD S.
Query Match 16.1%; Score 290.5; DB 8; Length 5636;
Best Local Similarity 31.1%; Pred. No. 1.3e-14;
RESULT 689
ID ADK60506 standard; protein; 5636 AA.
DE Angiogenesis differentially expressed protein GS-P29.
PN FR2836686-A1.
PD 05-SEP-2003.
PA (GENE-) GENE SIGNAL.
PA (ALMA/) AL MAHMOOD S.
Query Match 16.1%; Score 290.5; DB 8; Length 5636;
Best Local Similarity 31.1%; Pred. No. 1.3e-14;
RESULT 690
ID ADP73129 standard; protein; 5636 AA.
DE Angiogenesis inhibitor human protein sequence, GS-P29.

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PN FR2843753-A1.
 PD 27-FEB-2004.
 PA (GENE//) GENE S.
 PA (ALMS//) AL M S.
 Query Match 16.1%; Score 280.5; DB 8; Length 5636;
 Best Local Similarity 31.1%; Pred. No. 1.3e-14;
 RESULT 691
 ID ADG39844 standard; protein; 1708 AA.
 DE Protein similar to human NOV9 #5.
 PN US2003203843-A1.
 PD 30-OCT-2003.
 PA (PENA//) PENA C E A.
 PA (GUOX//) GUO X.
 PA (SHIM//) SHIMKETS R A.
 PA (PADI//) PADIGARU M.
 PA (KEKU//) KEKUDA R.
 PA (SPYT//) SPYTEK K A.
 PA (MEHR//) MEHRABAN F.
 PA (TOPP//) TOPPER J N.
 PA (MALY//) MALYANKAR U M.
 PA (WASS//) WASSERMAN S M.
 PA (EDIN//) EDINGER S R.
 PA (SMIT//) SMITHSON G.
 PA (GUNT//) GUNTHER E.
 PA (KOMU//) KOMUVES L.
 Query Match 16.0%; Score 289.5; DB 7; Length 1708;
 Best Local Similarity 29.8%; Pred. No. 3e-15;
 RESULT 692
 ID ADG39840 standard; protein; 1708 AA.
 DE Protein similar to human NOV9 #1.
 PN US2003203843-A1.
 PD 30-OCT-2003.
 PA (PENA//) PENA C E A.
 PA (GUOX//) GUO X.
 PA (SHIM//) SHIMKETS R A.
 PA (PADI//) PADIGARU M.
 PA (KEKU//) KEKUDA R.
 PA (SPYT//) SPYTEK K A.
 PA (MEHR//) MEHRABAN F.
 PA (TOPP//) TOPPER J N.
 PA (MALY//) MALYANKAR U M.
 PA (WASS//) WASSERMAN S M.
 PA (EDIN//) EDINGER S R.
 PA (SMIT//) SMITHSON G.
 PA (GUNT//) GUNTHER E.
 PA (KOMU//) KOMUVES L.
 Query Match 16.0%; Score 288.5; DB 6; Length 707;
 Best Local Similarity 31.1%; Pred. No. 1.1e-15;
 RESULT 693
 ID ABU69134 standard; protein; 707 AA.
 DE Human NOVX polypeptide #9.
 PN WO200290504-A2.
 PD 14-NOV-2002.
 PA (CURA-) CURAGEN CORP.
 Query Match 16.0%; Score 288.5; DB 6; Length 707;
 Best Local Similarity 31.1%; Pred. No. 1.1e-15;
 RESULT 694
 ID ADH72102 standard; protein; 707 AA.
 DE Human protein of the invention NOV43a SEQ ID NO:998.
 PN WO2003102155-A2.
 PD 11-DEC-2003.
 PA (CURA-) CURAGEN CORP.
 Query Match 16.0%; Score 288.5; DB 8; Length 707;
 Best Local Similarity 31.1%; Pred. No. 1.1e-15;
 RESULT 695
 ID ADO08271 standard; protein; 707 AA.
 DE Human NOVX polypeptide #9.
 PN US2004018594-A1.
 PD 29-JAN-2004.
 PA (ALSO//) ALSOBROOK J P.
 PA (ANDE//) ANDERSON D W.
 PA (BOLD//) BOLDOG F L.
 PA (BURG//) BURGESS C E.

PA (CASM//) CASMAN S J.
 PA (CHAP//) CHAPOVAL A.
 PA (EDIN//) EDINGER S R.
 PA (GERL//) GERLACH V.
 PA (GORM//) GORMAN L.
 PA (GUNT//) GUNTHER E.
 PA (GUOX//) GUO X S.
 PA (KEKU//) KEKUDA R.
 PA (LEPL//) LEPLEY D M.
 PA (LILL//) LI L.
 PA (LIOX//) LIU X.
 PA (MALY//) MALYANKAR U M.
 PA (MILL//) MILLER C E.
 PA (MILL//) MILLET I.
 PA (PADI//) PADIGARU M.
 PA (PATT//) PATTURAJAN M.
 PA (PENA//) PENA C E A.
 PA (RIEG//) RIEGER D K.
 PA (SHEN//) SHENOY S G.
 PA (SHIM//) SHIMKETS R A.
 PA (SPYT//) SPYTEK K A.
 PA (TAUP//) TAUPIER R J.
 PA (VERN//) VERNET C A M.
 PA (VOSS//) VOSS E Z.
 PA (ZERH//) ZERHUSEN B D.
 Query Match 16.0%; Score 288.5; DB 8; Length 707;
 Best Local Similarity 31.1%; Pred. No. 1.1e-15;
 RESULT 696
 ID ADH72104 standard; protein; 712 AA.
 DE Human protein of the invention NOV43b SEQ ID NO:1000.
 PN WO2003102155-A2.
 PD 11-DEC-2003.
 PA (CURA-) CURAGEN CORP.
 Query Match 16.0%; Score 288.5; DB 8; Length 712;
 Best Local Similarity 31.1%; Pred. No. 1.1e-15;
 RESULT 697
 ID ABU99129 standard; protein; 961 AA.
 DE Novel human GPCR related protein NOV9b.
 PN WO200299116-A2.
 PD 12-DEC-2002.
 PA (CURA-) CURAGEN CORP.
 Query Match 16.0%; Score 288.5; DB 6; Length 961;
 Best Local Similarity 30.5%; Pred. No. 1.7e-15;
 RESULT 698
 ID ADM93823 standard; protein; 961 AA.
 DE Human NOV protein #21.
 PN US2004009480-A1.
 PD 15-JAN-2004.
 PA (ANDE//) ANDERSON D W.
 PA (BAUM//) BAUMGARTNER J C.
 PA (BOLD//) BOLDOG F L.
 PA (CASM//) CASMAN S J.
 PA (EDIN//) EDINGER S R.
 PA (GANG//) GANGOLLI E A.
 PA (GERL//) GERLACH V.
 PA (GORM//) GORMAN L.
 PA (GUOX//) GUO X S.
 PA (HUAL//) HUALT T.
 PA (KEKU//) KEKUDA R.
 PA (LILL//) LI L.
 PA (MACD//) MACDOUGALL J R.
 PA (MALY//) MALYANKAR U M.
 PA (MILL//) MILLET I.
 PA (PADI//) PADIGARU M.
 PA (PATT//) PATTURAJAN M.
 PA (PENA//) PENA C E A.
 PA (RASI//) RASTELLI L.
 PA (SHIM//) SHIMKETS R A.
 PA (STON//) STONE D J.
 PA (SPYT//) SPYTEK K A M.
 PA (VERN//) VERNET C A M.
 PA (VOSS//) VOSS E Z.
 PA (ZERH//) ZERHUSEN B D.

ID AEB94406 standard; protein; 5622 AA.
 DE Human hemocentin/FIBL-6 protein, SEQ ID NO: 128.
 PN US2005176662-A1.
 PD 11-AUG-2005.
 PA (UYMI-) UNIV MIAMI.
 Query Match 16.0%; Score 288.5; DB 9; Length 5622;
 Best Local Similarity 31.1%; Pred. No. 1.9e-14;
 RESULT 711
 ID ABP60991 standard; protein; 5635 AA.
 DE Novel human protein. SEQ ID 78.
 PN WO200250105-A1.
 PD 27-JUN-2002.
 PA (SMIK) SMITHKLINE BEECHAM CORP.
 PA (SMIK) SMITHKLINE BEECHAM PLC.
 PA (GLAX) GLAXO GROUP LTD.
 Query Match 16.0%; Score 288.5; DB 5; Length 5635;
 Best Local Similarity 31.1%; Pred. No. 1.9e-14;
 RESULT 712
 ID AEC36829 standard; protein; 5636 AA.
 DE Human fibulin-6.
 PN WO2005083126-A2.
 PD 09-SEP-2005.
 PA (IOWA) UNIV IOWA RES FOUND.
 Query Match 16.0%; Score 288.5; DB 9; Length 5636;
 Best Local Similarity 31.1%; Pred. No. 1.9e-14;
 RESULT 713
 ID ADG39841 standard; protein; 1708 AA.
 DE Protein similar to human NOV9 #2.
 PN US2003203843-A1.
 PD 30-OCT-2003.
 PA (PENA) PENNA C E A.
 PA (GUOX) GUO X.
 PA (SHIM) SHIMKETS R A.
 PA (PADI) PADIGARU M.
 PA (KEKU) KEKUDA R.
 PA (SPYT) SPYTEK K A.
 PA (MEHR) MEHRABAN F.
 PA (TOPP) TOPPER J N.
 PA (MALY) MALYANKAR U M.
 PA (WASS) WASSERMAN S M.
 PA (EDIN) EDINGER S R.
 PA (SMIT) SMITHSON G.
 PA (GUNT) GUNTHER E.
 PA (KOMU) KOMUVES L.
 Query Match 15.9%; Score 287.5; DB 7; Length 1708;
 Best Local Similarity 31.1%; Pred. No. 4.5e-15;
 RESULT 714
 ID ADS98072 standard; protein; 1353 AA.
 DE Protein factor discovery related isolated human polypeptide, SEQ ID 336.
 PN WO2004087874-A2.
 PD 14-OCT-2004.
 PA (DRMA) DRMANAC R T.
 Query Match 15.8%; Score 285; DB 8; Length 1353;
 Best Local Similarity 28.8%; Pred. No. 5.4e-15;
 RESULT 715
 ID AB863044 standard; protein; 467 AA.
 DE Drosophila melanogaster polypeptide SEQ ID NO 15924.
 PN WO200171042-A2.
 PD 27-SEP-2001.
 PA (PEKE) PE CORP NY.
 Query Match 15.8%; Score 284.5; DB 4; Length 467;
 Best Local Similarity 26.1%; Pred. No. 1.4e-15;
 RESULT 716
 ID ADE63330 standard; protein; 858 AA.
 DE Rat Protein P13596, SEQ ID NO 9268.
 PN WO2003016475-A2.
 PD 27-FEB-2003.
 PA (GEHO) GEN HOSPITAL CORP.
 PA (FARB) BAYER AG.
 Query Match 15.4%; Score 277.5; DB 7; Length 858;
 Best Local Similarity 25.5%; Pred. No. 1.3e-14;
 RESULT 717

ID AD200014 standard; protein; 858 AA.
 DE Rat neural cell adhesion molecule (NCAM) protein SEQ ID NO:44.
 PN WO2005030804-A2.
 PD 07-APR-2005.
 PA (ENKA-) ENKAM PHARM AS.
 Query Match 15.4%; Score 277.5; DB 9; Length 858;
 Best Local Similarity 25.5%; Pred. No. 1.3e-14;
 RESULT 718
 ID ADA55624 standard; protein; 733 AA.
 DE Human protein, SEQ ID 3192.
 PN EPI293569-A2.
 PD 19-MAR-2003.
 PA (HELI-) HELIX RES INST.
 PA (REAS-) RES ASSOC BIOTECHNOLOGY.
 Query Match 15.3%; Score 276; DB 6; Length 733;
 Best Local Similarity 25.7%; Pred. No. 1.4e-14;
 RESULT 719
 ID ADE63332 standard; protein; 761 AA.
 DE Human Protein P13592, SEQ ID NO 9270.
 PN WO2003016475-A2.
 PD 27-FEB-2003.
 PA (GEHO) GEN HOSPITAL CORP.
 PA (FARB) BAYER AG.
 Query Match 15.3%; Score 276; DB 7; Length 761;
 Best Local Similarity 25.7%; Pred. No. 1.5e-14;
 RESULT 720
 ID AAY85655 standard; protein; 848 AA.
 DE Human NCAM 140kd isoform precursor amino acid sequence.
 PN WO200018801-A2.
 PD 06-APR-2000.
 PA (RONN) RONN L C B.
 PA (BOCK) BOCK E.
 PA (HOLM) HOLM A.
 PA (OLSE) OLSEN M.
 PA (OSTE) OSTERGAARD S.
 PA (JENS) JENSEN P H.
 PA (POUL) POULSEN F M.
 PA (SORO) SOROKA V.
 PA (RALE) RALETS I.
 PA (BERE) BEREZIN V.
 Query Match 15.3%; Score 276; DB 3; Length 848;
 Best Local Similarity 25.7%; Pred. No. 1.7e-14;
 RESULT 721
 ID AAE17222 standard; protein; 848 AA.
 DE Human 140kd NCAM isoform protein.
 PN WO200196364-A2.
 PD 20-DEC-2001.
 PA (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.
 PA (UNLO) KINGS COLLEGE LONDON.
 Query Match 15.3%; Score 276; DB 5; Length 848;
 Best Local Similarity 25.7%; Pred. No. 1.7e-14;
 RESULT 722
 ID AD124546 standard; protein; 848 AA.
 DE Human modifier of Chk1 (MCHK) protein SEQ ID NO:96.
 PN WO2004004785-A1.
 PD 15-JAN-2004.
 PA (EXEL-) EXELIXIS INC.
 Query Match 15.3%; Score 276; DB 8; Length 848;
 Best Local Similarity 25.7%; Pred. No. 1.7e-14;
 RESULT 723
 ID ADV70189 standard; protein; 848 AA.
 DE Tumor-associated antigenic target polypeptide TAT434.
 PN WO2004112829-A2.
 PD 29-DEC-2004.
 PA (GETH) GENENTECH INC.
 Query Match 15.3%; Score 276; DB 9; Length 848;
 Best Local Similarity 25.7%; Pred. No. 1.7e-14;
 RESULT 724
 ID ADZ26495 standard; protein; 848 AA.
 DE Human CD56.
 PN WO2005030999-A1.
 PD 07-APR-2005.
 PA (DAND) DANA FARBER CANCER INST INC.

Query Match 15.3%; Score 276; DB 9; Length 848;
 Best Local Similarity 25.7%; Pred. No. 1.7e-14;
 RESULT 725
 ID ADZ00015 standard; protein; 848 AA.
 DE Human neural cell adhesion molecule (NCAM) protein SEQ ID NO:45.
 PN W02005030804-A2.
 PD 07-APR-2005.
 PA (ENKA-) ENKAM PHARM AS.
 Query Match 15.3%; Score 276; DB 9; Length 848;
 Best Local Similarity 25.7%; Pred. No. 1.7e-14;
 RESULT 726
 ID ABE26423 standard; protein; 848 AA.
 DE Human CD56, variant 1, amino acid.
 PN W02005115456-A2.
 PD 08-DEC-2005.
 PA (HARD) HARVARD COLLEGE.
 Query Match 15.3%; Score 276; DB 10; Length 848;
 Best Local Similarity 25.7%; Pred. No. 1.7e-14;
 RESULT 727
 ID ADF28603 standard; protein; 853 AA.
 DE Bovine NCAM-140 protein - SED ID 513.
 PN W02003048326-A2.
 PD 12-JUN-2003.
 PA (HYSE-) HYSEQ INC.
 Query Match 15.3%; Score 275.5; DB 7; Length 853;
 Best Local Similarity 25.5%; Pred. No. 1.9e-14;
 RESULT 728
 ID ADL36019 standard; protein; 90 AA.
 DE Human NOVX-related polypeptide #17.
 PN US2003207800-A1.
 PD 06-NOV-2003.
 PA (MALY/) MALYANKAR U M.
 PA (SHEN/) SHENOY S G.
 PA (SPYT/) SPYTEK K A.
 PA (ZERH/) ZERHUSEN B D.
 PA (PATT/) PATTURAJAN M.
 PA (GUOX/) GUO X.
 PA (KEKU/) KEKUDA R.
 PA (GANG/) GANGOLLI E A.
 PA (SHIM/) SHIMKETS R A.
 PA (TAUP/) TAUPIER R J.
 PA (LILL/) LI L.
 PA (PADI/) PADIGARU M.
 Query Match 15.2%; Score 275; DB 7; Length 90;
 Best Local Similarity 61.8%; Pred. No. 9.6e-16;
 RESULT 729
 ID ADD25619 standard; protein; 848 AA.
 DE Binding domain-immunoglobulin fusion protein-associated protein #87.
 PN US2003118592-A1.
 PD 26-JUN-2003.
 PA (GENE-) GENE-CRAFT INC.
 Query Match 15.2%; Score 275; DB 7; Length 848;
 Best Local Similarity 25.7%; Pred. No. 2.1e-14;
 RESULT 730
 ID ADW95933 standard; protein; 848 AA.
 DE Human CD56.
 PN W02005011524-A1.
 PD 10-FEB-2005.
 PA (CARD-) CARDIO INC.
 Query Match 15.2%; Score 275; DB 9; Length 848;
 Best Local Similarity 25.7%; Pred. No. 2.1e-14;
 RESULT 731
 ID ADX15799 standard; protein; 848 AA.
 DE Human CD56.
 PN W02005012512-A1.
 PD 10-FEB-2005.
 PA (NAKA/) NAKAMURA N.
 Query Match 15.2%; Score 275; DB 9; Length 848;
 Best Local Similarity 25.7%; Pred. No. 2.1e-14;
 RESULT 732
 ID AAB37177 standard; protein; 1477 AA.
 DE Human LRRCAPS protein #2.
 PN W02003035831-A2.

PD 01-MAY-2003.
 PA (EXEL-) EXELIXIS INC.
 Query Match 15.2%; Score 274; DB 6; Length 1477;
 Best Local Similarity 29.2%; Pred. No. 5.4e-14;
 RESULT 733
 ID ADH48824 standard; protein; 1356 AA.
 DE NOV45B protein sequence, SEQ ID 108.
 PN W0200268652-A2.
 PD 06-SEP-2002.
 PA (CURA-) CURAGEN CORP.
 Query Match 15.1%; Score 273.5; DB 5; Length 1356;
 Best Local Similarity 29.6%; Pred. No. 5.3e-14;
 RESULT 734
 ID ADH48822 standard; protein; 1426 AA.
 DE NOV45A protein sequence, SEQ ID 106.
 PN W0200268652-A2.
 PD 06-SEP-2002.
 PA (CURA-) CURAGEN CORP.
 Query Match 15.0%; Score 271.5; DB 5; Length 1426;
 Best Local Similarity 29.6%; Pred. No. 8.4e-14;
 RESULT 735
 ID ADZ26717 standard; protein; 858 AA.
 DE Human CD56.
 PN W02005030999-A1.
 PD 07-APR-2005.
 PA (DAND) DANA FARBBER CANCER INST INC.
 Query Match 15.0%; Score 271; DB 9; Length 858;
 Best Local Similarity 24.8%; Pred. No. 4.6e-14;
 RESULT 736
 ID AEE26425 standard; protein; 858 AA.
 DE Human CD56, variant 2, amino acid.
 PN W02005115456-A2.
 PD 08-DEC-2005.
 PA (HARD) HARVARD COLLEGE.
 Query Match 15.0%; Score 271; DB 10; Length 858;
 Best Local Similarity 24.8%; Pred. No. 4.6e-14;
 RESULT 737
 ID RAO30845 standard; protein; 859 AA.
 DE Human cell adhesion and extracellular matrix protein (CADSCM)-35.
 PN W02003047526-A2.
 PD 12-JUN-2003.
 PA (INCY-) INCVTE GENOMICS INC.
 Query Match 15.0%; Score 271; DB 7; Length 859;
 Best Local Similarity 24.8%; Pred. No. 4.6e-14;
 RESULT 738
 ID ABB68566 standard; protein; 729 AA.
 DE Drosophila melanogaster polypeptide SEQ ID NO 32490.
 PN W0200171042-A2.
 PD 27-SEP-2001.
 PA (PEKE) PE CORP NY.
 Query Match 15.0%; Score 270; DB 4; Length 729;
 Best Local Similarity 26.7%; Pred. No. 4.5e-14;
 RESULT 739
 ID AAU18023 standard; protein; 152 AA.
 DE Human immunoglobulin polypeptide SEQ ID NO 168.
 PN W0200155315-A2.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 14.9%; Score 269; DB 4; Length 152;
 Best Local Similarity 42.3%; Pred. No. 6.5e-15;
 RESULT 740
 ID ADB31647 standard; protein; 152 AA.
 DE Human novel protein SEQ ID NO 168.
 PN US2003077606-A1.
 PD 24-APR-2003.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 14.9%; Score 269; DB 7; Length 152;
 Best Local Similarity 42.3%; Pred. No. 6.5e-15;
 RESULT 741
 ID ADR66889 standard; protein; 1469 AA.
 DE Human prostatic carcinoma derived DNA SEQ ID 187 #4.
 PN W02004076614-A2.
 PD 10-SEP-2004.

PA (HINZ/) HINZMANN B. 14.9%; Score 268.5; DB 8; Length 1469;
 PA (DAHL/) DAHL E. 28.8%; Pred. No. 1.6e-13;
 PA (ROSE/) ROSENTHAL A. 14.9%; Score 268.5; DB 8; Length 1469;
 PA (HERM/) HERMANN K. 28.8%; Pred. No. 1.6e-13;
 PA (PILA/) PILARSKY C. 14.9%; Score 268.5; DB 8; Length 1469;
 Query Match 28.8%; Pred. No. 1.6e-13;
 Best Local Similarity 28.8%; Pred. No. 1.6e-13;
 RESULT 742
 ID ADR65991 standard; protein; 1469 AA.
 DE Human prostatic carcinoma derived protein SEQ ID 187 #1.
 PN WO2004076614-A2.
 PD 10-SEP-2004.
 PA (HINZ/) HINZMANN B. 14.9%; Score 268.5; DB 8; Length 1469;
 PA (DAHL/) DAHL E. 28.8%; Pred. No. 1.6e-13;
 PA (ROSE/) ROSENTHAL A. 14.9%; Score 268.5; DB 8; Length 1469;
 PA (HERM/) HERMANN K. 28.8%; Pred. No. 1.6e-13;
 PA (PILA/) PILARSKY C. 14.9%; Score 268.5; DB 8; Length 1469;
 Query Match 28.8%; Pred. No. 1.6e-13;
 Best Local Similarity 28.8%; Pred. No. 1.6e-13;
 RESULT 743
 ID ADL35717 standard; protein; 1479 AA.
 DE Human peroxidase-melanoma antigen-related protein.
 PN WO2004019893-A2.
 PD 11-MAR-2004.
 PA (RIGE-) RIGEL PHARM INC. 14.9%; Score 268.5; DB 8; Length 1479;
 Query Match 28.8%; Pred. No. 1.6e-13;
 Best Local Similarity 28.8%; Pred. No. 1.6e-13;
 RESULT 744
 ID AAW81030 standard; protein; 1496 AA.
 DE Melanoma associated antigen MG50.
 PN WO9855133-A1.
 PD 10-DEC-1998.
 PA (REGC-) UNIV CALIFORNIA. 14.9%; Score 268.5; DB 2; Length 1496;
 PA (UYSC-) UNIV SOUTHERN CALIFORNIA. 28.8%; Pred. No. 1.6e-13;
 Query Match 28.8%; Pred. No. 1.6e-13;
 Best Local Similarity 28.8%; Pred. No. 1.6e-13;
 RESULT 745
 ID AAY70469 standard; protein; 1496 AA.
 DE Human p53 target molecule, PRG2 protein.
 PN WO200012526-A1.
 PD 09-MAR-2000.
 PA (UYPR-) UNIV PRINCETON. 14.9%; Score 268.5; DB 3; Length 1496;
 Query Match 28.8%; Pred. No. 1.6e-13;
 Best Local Similarity 28.8%; Pred. No. 1.6e-13;
 RESULT 746
 ID ABU03498 standard; protein; 1496 AA.
 DE Angiogenesis-associated human protein sequence #43.
 PN WO200279492-A2.
 PD 10-OCT-2002.
 PA (EOSB-) EOS BIOTECHNOLOGY INC. 14.9%; Score 268.5; DB 6; Length 1496;
 Query Match 28.8%; Pred. No. 1.6e-13;
 Best Local Similarity 28.8%; Pred. No. 1.6e-13;
 RESULT 747
 ID ADD89024 standard; protein; 1496 AA.
 DE TAT264.
 PN WO2003057160-A2.
 PD 17-JUL-2003.
 PA (GETH-) GENENTECH INC. 14.9%; Score 268.5; DB 7; Length 1496;
 Query Match 28.8%; Pred. No. 1.6e-13;
 Best Local Similarity 28.8%; Pred. No. 1.6e-13;
 RESULT 748
 ID ADF28706 standard; protein; 1496 AA.
 DE Human peroxidase-like MG50 protein - SEQ ID 616.
 PN WO2003048326-A2.
 PD 12-JUN-2003.
 PA (HYSE-) HYSEQ INC. 14.9%; Score 268.5; DB 7; Length 1496;
 Query Match 28.8%; Pred. No. 1.6e-13;
 Best Local Similarity 28.8%; Pred. No. 1.6e-13;
 RESULT 749
 ID ADQ18902 standard; protein; 1496 AA.
 DE Human soft tissue sarcoma-upregulated protein - SEQ ID 1721.
 PN WO2004048938-A2.
 PD 10-JUN-2004.

PA (PROT-) PROTEIN DESIGN LABS INC. 14.9%; Score 268.5; DB 8; Length 1496;
 Query Match 28.8%; Pred. No. 1.6e-13;
 Best Local Similarity 28.8%; Pred. No. 1.6e-13;
 RESULT 750
 ID ADQ89920 standard; protein; 1496 AA.
 DE Antagonist of cell cycle progression polypeptide #175.
 PN WO2004063362-A2.
 PD 29-JUL-2004.
 PA (CYCL-) CYCLACEL LTD. 14.9%; Score 268.5; DB 8; Length 1496;
 Query Match 28.8%; Pred. No. 1.6e-13;
 Best Local Similarity 28.8%; Pred. No. 1.6e-13;
 RESULT 751
 ID ADQ89914 standard; protein; 1496 AA.
 DE Antagonist of cell cycle progression polypeptide #172.
 PN WO2004063362-A2.
 PD 29-JUL-2004.
 PA (CYCL-) CYCLACEL LTD. 14.9%; Score 268.5; DB 8; Length 1496;
 Query Match 28.8%; Pred. No. 1.6e-13;
 Best Local Similarity 28.8%; Pred. No. 1.6e-13;
 RESULT 752
 ID ADR66092 standard; protein; 1496 AA.
 DE Human prostatic carcinoma derived protein SEQ ID 288 #1.
 PN WO2004076614-A2.
 PD 10-SEP-2004.
 PA (HINZ/) HINZMANN B. 14.9%; Score 268.5; DB 8; Length 1496;
 PA (DAHL/) DAHL E. 28.8%; Pred. No. 1.6e-13;
 PA (ROSE/) ROSENTHAL A. 14.9%; Score 268.5; DB 8; Length 1496;
 PA (HERM/) HERMANN K. 28.8%; Pred. No. 1.6e-13;
 PA (PILA/) PILARSKY C. 14.9%; Score 268.5; DB 8; Length 1496;
 Query Match 28.8%; Pred. No. 1.6e-13;
 Best Local Similarity 28.8%; Pred. No. 1.6e-13;
 RESULT 753
 ID ADR66434 standard; protein; 1496 AA.
 DE Human prostatic carcinoma derived protein SEQ ID 288 #2.
 PN WO2004076614-A2.
 PD 10-SEP-2004.
 PA (HINZ/) HINZMANN B. 14.9%; Score 268.5; DB 8; Length 1496;
 PA (DAHL/) DAHL E. 28.8%; Pred. No. 1.6e-13;
 PA (ROSE/) ROSENTHAL A. 14.9%; Score 268.5; DB 8; Length 1496;
 PA (HERM/) HERMANN K. 28.8%; Pred. No. 1.6e-13;
 PA (PILA/) PILARSKY C. 14.9%; Score 268.5; DB 8; Length 1496;
 Query Match 28.8%; Pred. No. 1.6e-13;
 Best Local Similarity 28.8%; Pred. No. 1.6e-13;
 RESULT 754
 ID ABH11587 standard; peptide; 1498 AA.
 DE Human peroxidase homologue, SEQ ID NO:1957.
 PN WO200157188-A2.
 PD 09-AUG-2001.
 PA (HYSE-) HYSEQ INC. 14.9%; Score 268.5; DB 4; Length 1498;
 Query Match 28.8%; Pred. No. 1.6e-13;
 Best Local Similarity 28.8%; Pred. No. 1.6e-13;
 RESULT 755
 ID ABO00762 standard; protein; 1498 AA.
 DE Polypeptide encoded by novel human contig #13.
 PN WO2003023013-A2.
 PD 20-MAR-2003.
 PA (HYSE-) HYSEQ INC. 14.9%; Score 268.5; DB 6; Length 1498;
 Query Match 28.8%; Pred. No. 1.6e-13;
 Best Local Similarity 28.8%; Pred. No. 1.6e-13;
 RESULT 756
 ID AAG02771 standard; protein; 58 AA.
 DE Human secreted protein, SEQ ID NO: 6852.
 PN EP1033401-A2.
 PD 06-SEP-2000.
 PA (GEST-) GENSET. 14.8%; Score 267; DB 3; Length 58;
 Query Match 86.2%; Pred. No. 2.6e-15;
 Best Local Similarity 86.2%; Pred. No. 2.6e-15;
 RESULT 757
 ID ADV97835 standard; protein; 36946 AA.
 DE Murine protein kinase enzyme Seq 155.
 PN WO2005000200-A2.
 PD 06-JAN-2005.
 PA (SUGE-) SUGEN INC.

Query Match 14.7%; Score 266; DB 9; Length 36946;
Best Local Similarity 27.6%; Pred. No. 2.1e-11;
RESULT 758
ID ABB97902 standard; protein; 142 AA.
DE Human secretory polypeptide (SPTM) 154.
PN WO200220756-A2.
PD 14-MAR-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 14.6%; Score 263; DB 5; Length 142;
Best Local Similarity 44.1%; Pred. No. 1.9e-14;
RESULT 759
ID AAY13563 standard; protein; 1395 AA.
DE Drosophila Robo 1 polypeptide.
PN WO925833-A1.
PD 27-MAY-1999.
PA (REGC) UNIV CALIFORNIA.
Query Match 14.5%; Score 261; DB 2; Length 1395;
Best Local Similarity 26.1%; Pred. No. 6.6e-13;
RESULT 760
ID AAY08401 standard; protein; 1395 AA.
DE Drosophila sp. Robo1 protein.
PN WO9920764-A1.
PD 29-APR-1999.
PA (REGC) UNIV CALIFORNIA.
Query Match 14.5%; Score 261; DB 2; Length 1395;
Best Local Similarity 26.1%; Pred. No. 6.6e-13;
RESULT 761
ID ADB85335 standard; protein; 1395 AA.
DE Fruitfly nerve cell growth modulator SLIT-1-associated sequence #1.
PN US2003170727-A1.
PD 11-SEP-2003.
PA (GOOD) GOODMAN C S.
PA (KIDD) KIDD T.
PA (BROS) BROSE K.
PA (TESS) TESSIER-LAVIGNE M.
Query Match 14.5%; Score 261; DB 7; Length 1395;
Best Local Similarity 26.1%; Pred. No. 6.6e-13;
RESULT 762
ID ABB62052 standard; protein; 496 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 12948.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 14.4%; Score 260.5; DB 4; Length 496;
Best Local Similarity 26.2%; Pred. No. 1.8e-13;
RESULT 763
ID ABB68257 standard; protein; 1395 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 31563.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 14.4%; Score 260; DB 4; Length 1395;
Best Local Similarity 26.1%; Pred. No. 8e-13;
RESULT 764
ID AAY53666 standard; protein; 4412 AA.
DE Sequence gi/1017427/emb/CAA62189 from an alignment with protein 608.
PN WO9960164-A1.
PD 25-NOV-1999.
PA (QUAR-) QUARK BIOTECH INC.
Query Match 14.3%; Score 259; DB 3; Length 4412;
Best Local Similarity 29.6%; Pred. No. 4.7e-12;
RESULT 765
ID ABG74786 standard; protein; 31267 AA.
DE Human RGS11 protein.
PN WO2002103355-A1.
PD 27-DEC-2002.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 14.3%; Score 259; DB 6; Length 31267;
Best Local Similarity 29.6%; Pred. No. 6.9e-11;
RESULT 766
ID AD089964 standard; protein; 34350 AA.
DE Antagonist of cell cycle progression polypeptide #197.
PN WO2004063362-A2.

PD 29-JUL-2004.
PA (CYCL-) CYCLACEL LTD.
Query Match 14.3%; Score 259; DB 8; Length 34350;
Best Local Similarity 29.6%; Pred. No. 7.8e-11;
RESULT 767
ID ADM74171 standard; protein; 381 AA.
DE Human NOV3A protein sequence SeqID10.
PN WO2004015079-A2.
PD 19-FEB-2004.
PA (CURA-) CURAGEN CORP.
Query Match 14.3%; Score 258.5; DB 8; Length 381;
Best Local Similarity 27.4%; Pred. No. 1.8e-13;
RESULT 768
ID ADM56387 standard; protein; 404 AA.
DE Human cell adhesion molecule NOV12.
PN US2003082554-A1.
PD 01-MAY-2003.
PA (CURA-) CURAGEN CORP.
Query Match 14.2%; Score 256.5; DB 7; Length 404;
Best Local Similarity 27.4%; Pred. No. 2.9e-13;
RESULT 769
ID ADX44506 standard; protein; 421 AA.
DE Human beta-secretase protein fragment, seqid:1.
PN US6852482-B1.
PD 08-FEB-2005.
PA (ELAN-) ELAN PHARM INC.
Query Match 14.2%; Score 256; DB 9; Length 421;
Best Local Similarity 26.7%; Pred. No. 3.4e-13;
RESULT 770
ID AAY33741 standard; protein; 444 AA.
DE Beta-secretase.
PN US5942400-A.
PD 24-AUG-1999.
PA (ELAN-) ELAN PHARM INC.
Query Match 14.2%; Score 256; DB 2; Length 444;
Best Local Similarity 26.7%; Pred. No. 3.7e-13;
RESULT 771
ID AAB47251 standard; protein; 444 AA.
DE Beta-secretase.
PN US6221645-B1.
PD 24-APR-2001.
PA (ELAN-) ELAN PHARM INC.
Query Match 14.2%; Score 256; DB 4; Length 444;
Best Local Similarity 26.7%; Pred. No. 3.7e-13;
RESULT 772
ID ADX44510 standard; protein; 444 AA.
DE Human beta-secretase protein, seqid:5.
PN US6852482-B1.
PD 08-FEB-2005.
PA (ELAN-) ELAN PHARM INC.
Query Match 14.2%; Score 256; DB 9; Length 444;
Best Local Similarity 26.7%; Pred. No. 3.7e-13;
RESULT 773
ID ABB63920 standard; protein; 359 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 18552.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 14.1%; Score 255; DB 4; Length 359;
Best Local Similarity 24.9%; Pred. No. 3.4e-13;
RESULT 774
ID ADN24208 standard; protein; 5175 AA.
DE Bacterial polypeptide #6861.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOV) CAO Y.
PA (HINK) HINKLE G J.
PA (SLAT) SLATER S C.
PA (CHEN) CHEN X.
PA (GOLD) GOLDMAN B S.
Query Match 14.1%; Score 254.5; DB 8; Length 5175;
Best Local Similarity 29.3%; Pred. No. 1.4e-11;
RESULT 775

ID ADN24206 standard; protein; 5175 AA.
DE Bacterial polypeptide #6859.
PD US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 14.1%; Score 254.5; DB 8; Length 5175;
Best Local Similarity 29.3%; Pred. No. 1.4e-11;
RESULT 776
ID ADN24207 standard; protein; 5198 AA.
DE Bacterial polypeptide #6860.
PD US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 14.1%; Score 254.5; DB 8; Length 5198;
Best Local Similarity 29.3%; Pred. No. 1.4e-11;
RESULT 777
ID ADN24205 standard; protein; 5198 AA.
DE Bacterial polypeptide #6858.
PD US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 14.1%; Score 254.5; DB 8; Length 5198;
Best Local Similarity 29.3%; Pred. No. 1.4e-11;
RESULT 778
ID ADN74177 standard; protein; 306 AA.
DE Human NOV3D protein sequence SeqID16.
PD WO2004015079-A2.
PD 19-FEB-2004.
PA (CURA-) CURAGEN CORP.
Query Match 14.0%; Score 253.5; DB 8; Length 306;
Best Local Similarity 27.1%; Pred. No. 3.7e-13;
RESULT 779
ID ABG66677 standard; protein; 404 AA.
DE Human novel polypeptide #12.
PD WO200244340-A2.
PD 06-JUN-2002.
PA (HYSE-) HYSEQ INC.
Query Match 14.0%; Score 253.5; DB 5; Length 404;
Best Local Similarity 27.1%; Pred. No. 5.3e-13;
RESULT 780
ID ABJ20221 standard; protein; 404 AA.
DE Human IG gene related protein SEQ ID NO 44.
PD WO200299040-A2.
PD 12-DEC-2002.
PA (EXEL-) EXELIXIS INC.
Query Match 14.0%; Score 253.5; DB 6; Length 404;
Best Local Similarity 27.1%; Pred. No. 5.3e-13;
RESULT 781
ID ADP66751 standard; protein; 404 AA.
DE Novel human protein NOV12.
PD US2003199103-A1.
PD 23-OCT-2003.
PA (CURA-) CURAGEN CORP.
Query Match 14.0%; Score 253.5; DB 8; Length 404;
Best Local Similarity 27.1%; Pred. No. 5.3e-13;
RESULT 782
ID ADI19788 standard; protein; 404 AA.
DE Human NOV12 protein.
PD US2004002134-A1.
PD 01-JAN-2004.
PA (CURA-) CURAGEN CORP.
Query Match 14.0%; Score 253.5; DB 4; Length 404;
Best Local Similarity 27.1%; Pred. No. 2.8e-12;
RESULT 783
ID ADO60261 standard; protein; 404 AA.
DE Human NOV12 protein.
PD US2003134430-A1.
PD 17-JUL-2003.
PA (CURA-) CURAGEN CORP.
Query Match 14.0%; Score 253.5; DB 8; Length 404;
Best Local Similarity 27.1%; Pred. No. 5.3e-13;
RESULT 784
ID ADO47378 standard; protein; 568 AA.
DE Human neurotrophin-like protein-related protein SeqID13.
PD WO2004039942-A2.
PD 13-MAY-2004.
PA (NUVE-) NUVELO.
Query Match 14.0%; Score 253; DB 8; Length 568;
Best Local Similarity 27.4%; Pred. No. 9.4e-13;
RESULT 785
ID ABB76023 standard; protein; 570 AA.
DE Neurotrophin-like polypeptide.
PD WO200157175-A2.
PD 09-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match 14.0%; Score 253; DB 4; Length 570;
Best Local Similarity 27.4%; Pred. No. 9.4e-13;
RESULT 786
ID ABB76018 standard; protein; 586 AA.
DE Neurotrophin-like polypeptide splice variant.
PD WO200157175-A2.
PD 09-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match 14.0%; Score 253; DB 4; Length 586;
Best Local Similarity 27.4%; Pred. No. 9.8e-13;
RESULT 787
ID ADO47372 standard; protein; 586 AA.
DE Human neurotrophin-like protein SeqID7.
PD WO2004039942-A2.
PD 13-MAY-2004.
PA (NUVE-) NUVELO.
Query Match 14.0%; Score 253; DB 8; Length 586;
Best Local Similarity 27.4%; Pred. No. 9.8e-13;
RESULT 788
ID ABO23244 standard; protein; 404 AA.
DE Human breast tumour associated protein 47-like polypeptide NOV12.
PD US2003027158-A1.
PD 06-FEB-2003.
PA (CURA-) CURAGEN CORP.
Query Match 13.9%; Score 251.5; DB 6; Length 404;
Best Local Similarity 27.1%; Pred. No. 7.9e-13;
RESULT 789
ID AAB61142 standard; protein; 404 AA.
DE Human NOV12 protein.
PD WO200075321-A2.
PD 14-DEC-2000.
PA (CURA-) CURAGEN CORP.
Query Match 13.9%; Score 250.5; DB 4; Length 404;
Best Local Similarity 27.1%; Pred. No. 9.7e-13;
RESULT 790
ID ABB61502 standard; protein; 885 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 11298.
PD WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE-) PE CORP NY.
Query Match 13.9%; Score 250.5; DB 4; Length 885;
Best Local Similarity 26.5%; Pred. No. 2.8e-12;
RESULT 791
ID ABB76016 standard; protein; 374 AA.
DE Neurotrophin-like polypeptide.
PD WO200157175-A2.
PD 09-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match 13.8%; Score 250; DB 4; Length 374;

Best Local Similarity 27.7%; Pred. No. 9.6e-13;
RESULT 792
ID ADO47381 standard; protein; 374 AA.
DE Human neurotrophin-like protein-related protein SeqID16.
PN WO2004039942-A2.
PD 13-MAY-2004.
PA (NUVE-) NUVELO.
Query Match 13.8%; Score 250; DB 8; Length 374;
Best Local Similarity 27.7%; Pred. No. 9.6e-13;
RESULT 793
ID ADO47377 standard; protein; 440 AA.
DE Human neurotrophin-like protein-related protein SeqID12.
PN WO2004039942-A2.
PD 13-MAY-2004.
PA (NUVE-) NUVELO.
Query Match 13.8%; Score 250; DB 8; Length 440;
Best Local Similarity 27.7%; Pred. No. 1.2e-12;
RESULT 794
ID ABB76022 standard; protein; 442 AA.
DE Neurotrophin-like polypeptide.
PN WO200157175-A2.
PD 09-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match 13.8%; Score 250; DB 4; Length 442;
Best Local Similarity 27.7%; Pred. No. 1.2e-12;
RESULT 795
ID ABB76017 standard; protein; 458 AA.
DE Neurotrophin-like polypeptide.
PN WO200157175-A2.
PD 09-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match 13.8%; Score 250; DB 4; Length 458;
Best Local Similarity 27.7%; Pred. No. 1.3e-12;
RESULT 796
ID ADO47369 standard; protein; 458 AA.
DE Human neurotrophin-like protein SeqID4.
PN WO2004039942-A2.
PD 13-MAY-2004.
PA (NUVE-) NUVELO.
Query Match 13.8%; Score 250; DB 8; Length 458;
Best Local Similarity 27.7%; Pred. No. 1.3e-12;
RESULT 797
ID ADS10607 standard; protein; 458 AA.
DE Human therapeutic protein - SEQ ID 844.
PN WO2004080148-A2.
PD 23-SEP-2004.
PA (NUVE-) NUVELO INC.
Query Match 13.8%; Score 250; DB 8; Length 458;
Best Local Similarity 27.7%; Pred. No. 1.3e-12;
RESULT 798
ID ADO47385 standard; protein; 880 AA.
DE Human neurotrophin-like protein-related protein SeqID13.
PN WO2004039942-A2.
PD 13-MAY-2004.
PA (NUVE-) NUVELO.
Query Match 13.8%; Score 250; DB 8; Length 880;
Best Local Similarity 27.7%; Pred. No. 3.1e-12;
RESULT 799
ID AAO30844 standard; protein; 886 AA.
DE Human cell adhesion and extracellular matrix protein (CADECM)-34.
PN WO2003047526-A2.
PD 12-JUN-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 13.8%; Score 250; DB 7; Length 886;
Best Local Similarity 27.7%; Pred. No. 3.1e-12;
RESULT 800
ID ADO47396 standard; protein; 955 AA.
DE Human neurotrophin-like protein-related MAM domain GPIM protein SeqID31.
PN WO2004039942-A2.
PD 13-MAY-2004.
PA (NUVE-) NUVELO.
Query Match 13.8%; Score 250; DB 8; Length 955;
Best Local Similarity 27.7%; Pred. No. 3.5e-12;
RESULT 801
ID ADO47383 standard; protein; 955 AA.
DE Human neurotrophin-like protein SeqID18.
PN WO2004039942-A2.
PD 13-MAY-2004.
PA (NUVE-) NUVELO.
Query Match 13.8%; Score 250; DB 8; Length 955;
Best Local Similarity 27.7%; Pred. No. 3.5e-12;
RESULT 802
ID ADS10608 standard; protein; 955 AA.
DE Human therapeutic protein - SEQ ID 845.
PN WO2004080148-A2.
PD 23-SEP-2004.
PA (NUVE-) NUVELO INC.
Query Match 13.8%; Score 250; DB 8; Length 955;
Best Local Similarity 27.7%; Pred. No. 3.5e-12;
RESULT 803
ID ADS11107 standard; protein; 970 AA.
DE Human therapeutic protein - SEQ ID 1344.
PN WO2004080148-A2.
PD 23-SEP-2004.
PA (NUVE-) NUVELO INC.
Query Match 13.8%; Score 250; DB 8; Length 970;
Best Local Similarity 27.7%; Pred. No. 3.5e-12;
RESULT 804
ID ABG12100 standard; protein; 1219 AA.
DE Novel human diagnostic protein #12091.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 13.8%; Score 250; DB 4; Length 1219;
Best Local Similarity 27.7%; Pred. No. 4.8e-12;
RESULT 805
ID ABUS2336 standard; protein; 1315 AA.
DE Human GPCR related protein NOV13a.
PN WO200279398-A2.
PD 10-OCT-2002.
PA (CURA-) CURAGEN CORP.
Query Match 13.8%; Score 250; DB 6; Length 1315;
Best Local Similarity 27.7%; Pred. No. 5.4e-12;
RESULT 806
ID ADH72138 standard; protein; 1315 AA.
DE Human protein of the invention NOV46h SEQ ID NO:1034.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 13.8%; Score 250; DB 8; Length 1315;
Best Local Similarity 27.7%; Pred. No. 5.4e-12;
RESULT 807
ID ADL24007 standard; protein; 1315 AA.
DE Human NOVX polypeptide #26.
PN US2004002120-A1.
PD 01-JAN-2004.
PA (KEKU/) KEKUDA R.
PA (TCHE/) TCHERNEV V T.
PA (LIUX/) LIU X.
PA (SPYI/) SPYTEK K A.
PA (PATT/) PATTURAJAN M.
PA (BURG/) BURGESS C E.
PA (VERN/) VERNET C A M.
PA (LILL/) LI L.
PA (GORM/) GORMAN L.
PA (MALI/) MALYANKAR U M.
PA (BOLD/) BOLDOGF F L.
PA (GUOX/) GUO X.
PA (SHEN/) SHENOY S G.
PA (PADI/) PADIGARU M.
PA (TAUP/) TAUPIER R J.
PA (MILL/) MILLER C E.
PA (CASM/) CASMAN S J.
PA (PENA/) PENNA C E A.
PA (GANG/) GANGOLLI E A.
PA (GUSE/) GUSEV V Y.

PA (SMIT/) SMITHSON G.
PA (ZERR/) ZERHUSEN B D.
PA (GERL/) GERLACH V.
PA (POCH/) POCHART P F.
PA (FERN/) FERNANDES E R.
PA (SHIM/) SHIMKETS R A.
PA (RAST/) RASTELLI L.
PA (SPAD/) SPADERNA S K.
PA (LARO/) LAROCHELLE W J.
PA (ZHON/) ZHONG M.
PA (KHRA/) KHRAMTSOV N V.
PA (VOSS/) VOSS E Z.
PA (HERR/) HERRMANN J L.
Query Match 13.8%; Score 250; DB 8; Length 1315;
Best Local Similarity 27.7%; Pred. No. 5.4e-12;
RESULT 808
ID ADH72134 standard; protein; 1335 AA.
DE Human protein of the invention NOV46f SEQ ID NO:1030.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 13.8%; Score 250; DB 8; Length 1335;
Best Local Similarity 27.7%; Pred. No. 5.5e-12;
RESULT 809
ID ABUS2329 standard; protein; 1386 AA.
DE Human GPCR related protein NOV12a.
PN WO200279398-A2.
PD 10-OCT-2002.
PA (CURA-) CURAGEN CORP.
Query Match 13.8%; Score 250; DB 6; Length 1386;
Best Local Similarity 27.7%; Pred. No. 5.8e-12;
RESULT 810
ID ADL23993 standard; protein; 1386 AA.
DE Human NOVX polypeptide #19.
PN US2004002120-A1.
PD 01-JAN-2004.
PA (KEKU/) KEKUDA R.
PA (TCH/) TCHERNEV V T.
PA (LIUX/) LIU X.
PA (SPYT/) SPYTEK K A.
PA (PAT/) PATTURAJAN M.
PA (BURG/) BURGESS C E.
PA (VERN/) VERNET C A M.
PA (LIL/) LI L.
PA (GORM/) GORMAN L.
PA (MALY/) MALYANKAR U M.
PA (BOLD/) BOLDYGO F L.
PA (GUOX/) GUO X.
PA (SHEN/) SHENOV S G.
PA (PADI/) PADIGARU M.
PA (TAUP/) TAUPIER R J.
PA (MILL/) MILLER C E.
PA (CASM/) CASMAN S J.
PA (PENA/) PENA C E A.
PA (GANG/) GANGOLLI E A.
PA (GUSE/) GUSEV V Y.
PA (SMIT/) SMITHSON G.
PA (ZERR/) ZERHUSEN B D.
PA (GERL/) GERLACH V.
PA (POCH/) POCHART P F.
PA (FERN/) FERNANDES E R.
PA (SHIM/) SHIMKETS R A.
PA (RAST/) RASTELLI L.
PA (SPAD/) SPADERNA S K.
PA (LARO/) LAROCHELLE W J.
PA (ZHON/) ZHONG M.
PA (KHRA/) KHRAMTSOV N V.
PA (VOSS/) VOSS E Z.
PA (HERR/) HERRMANN J L.
Query Match 13.8%; Score 250; DB 8; Length 1386;
Best Local Similarity 27.7%; Pred. No. 5.8e-12;
RESULT 811
ID ADD47172 standard; protein; 1040 AA.

DE Human Protein NP_005067, SEQ ID NO 12865.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 13.8%; Score 249.5; DB 7; Length 1040;
Best Local Similarity 26.1%; Pred. No. 4.3e-12;
RESULT 812
ID ADO28581 standard; protein; 1040 AA.
DE Human axonin-1 precursor (AXO1) protein SEQ ID NO:10.
PN WO2004044178-A2.
PD 27-MAY-2004.
PA (GETH) GENENTECH INC.
Query Match 13.8%; Score 249.5; DB 8; Length 1040;
Best Local Similarity 26.1%; Pred. No. 4.3e-12;
RESULT 813
ID ABO84729 standard; protein; 1040 AA.
DE Human cancer-associated protein HP22-025.2.
PN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 13.8%; Score 249.5; DB 8; Length 1040;
Best Local Similarity 26.1%; Pred. No. 4.3e-12;
RESULT 814
ID ABO84728 standard; protein; 1040 AA.
DE Human cancer-associated protein HP22-025.1.
PN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 13.8%; Score 249.5; DB 8; Length 1040;
Best Local Similarity 26.1%; Pred. No. 4.3e-12;
RESULT 815
ID ABB68882 standard; protein; 467 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 33438.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 13.7%; Score 248; DB 4; Length 467;
Best Local Similarity 27.4%; Pred. No. 1.9e-12;
RESULT 816
ID ADJ68312 standard; protein; 1007 AA.
DE Human heat mitochondrial protein as a therapeutic target SeqID118.
PN WO2003087768-A2.
PD 23-OCT-2003.
PA (MITO-) MITOKOR.
PA (BUCK-) BUCK INST AGE RES.
Query Match 13.6%; Score 246.5; DB 7; Length 1007;
Best Local Similarity 24.6%; Pred. No. 7.5e-12;
RESULT 817
ID AAR63759 standard; protein; 1018 AA.
DE Human contactin (EMBL Accession #Z21488).
PN EP618293-A1.
PD 05-OCT-1994.
PA (BECT) BECTON DICKINSON CO.
Query Match 13.6%; Score 246.5; DB 2; Length 1018;
Best Local Similarity 24.6%; Pred. No. 7.6e-12;
RESULT 818
ID AAR87028 standard; protein; 1018 AA.
DE Human contactin.
PN WO9535373-A2.
PD 28-DEC-1995.
PA (LJOL-) LA JOLLA CANCER RES FOUND.
Query Match 13.6%; Score 246.5; DB 2; Length 1018;
Best Local Similarity 24.6%; Pred. No. 7.6e-12;
RESULT 819
ID ADE71113 standard; protein; 1018 AA.
DE Contactin, SEQ ID 67.
PN WO2003070889-A2.
PD 28-AUG-2003.
PA (IDEC-) IDEC PHARM CORP.
Query Match 13.6%; Score 246.5; DB 7; Length 1018;
Best Local Similarity 24.6%; Pred. No. 7.6e-12;
RESULT 820

ID ADJ75696 standard; protein; 1018 AA.
DE Marker gene related amino acid sequence SEQ ID NO:948.
PN EPI394274-A2.
PD 03-MAR-2004.
PA (GENO-) GENOX RES INC.
Query Match 13.6%; Score 246.5; DB 8; Length 1018;
Best Local Similarity 24.6%; Pred. No. 7.6e-12;
RESULT 821
ID ADO28659 standard; protein; 1018 AA.
DE Human CONT protein SEQ ID NO:88.
PN WO2004044178-A2.
PD 27-MAY-2004.
PA (GETH) GENENTECH INC.
Query Match 13.6%; Score 246.5; DB 8; Length 1018;
Best Local Similarity 24.6%; Pred. No. 7.6e-12;
RESULT 822
ID ADP67246 standard; protein; 1018 AA.
DE Human P3/Contactin protein.
PN WO2004052389-A2.
PD 24-JUN-2004.
PA (SIGE-) SINGAPORE GEN HOSPITAL PTE LTD.
PA (FORR/) FORREST G R.
Query Match 13.6%; Score 246.5; DB 8; Length 1018;
Best Local Similarity 24.6%; Pred. No. 7.6e-12;
RESULT 823
ID ADR66068 standard; protein; 1073 AA.
DE Human prostatic carcinoma derived protein SEQ ID 264 #1.
PN WO2004076614-A2.
PD 10-SEP-2004.
PA (HINZ/) HINZMANN B.
PA (DAHL/) DAHL E.
PA (ROSE/) ROSENTHAL A.
PA (HERM/) HERMANN K.
PA (PILA/) PILARSKY C.
Query Match 13.6%; Score 245.5; DB 8; Length 1073;
Best Local Similarity 26.4%; Pred. No. 9.9e-12;
RESULT 824
ID ADR66410 standard; protein; 1073 AA.
DE Human prostatic carcinoma derived protein SEQ ID 264 #2.
PN WO2004076614-A2.
PD 10-SEP-2004.
PA (HINZ/) HINZMANN B.
PA (DAHL/) DAHL E.
PA (ROSE/) ROSENTHAL A.
PA (HERM/) HERMANN K.
PA (PILA/) PILARSKY C.
Query Match 13.6%; Score 245.5; DB 8; Length 1073;
Best Local Similarity 26.4%; Pred. No. 9.9e-12;
RESULT 825
ID ADA54925 standard; protein; 512 AA.
DE Human protein, SEQ ID 2493.
PN EPI293569-A2.
PD 19-MAR-2003.
PA (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 13.5%; Score 244.5; DB 6; Length 512;
Best Local Similarity 27.8%; Pred. No. 4.4e-12;
RESULT 826
ID AAW06485 standard; peptide; 1018 AA.
DE Rat contactin ligand for RPTbeta.
PN WO9637776-A1.
PD 28-NOV-1996.
PA (SUGE-) SUGEN INC.
Query Match 13.5%; Score 243.5; DB 2; Length 1018;
Best Local Similarity 24.0%; Pred. No. 1.4e-11;
RESULT 827
ID ADE56173 standard; protein; 1021 AA.
DE Rat Protein O63198, SEQ ID NO 2022.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 13.5%; Score 243.5; DB 7; Length 1021;
Best Local Similarity 27.0%; Pred. No. 6.6e-11;
RESULT 828
ID ABG03059 standard; protein; 792 AA.
DE Novel human diagnostic protein #3050.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 13.4%; Score 242.5; DB 4; Length 792;
Best Local Similarity 26.4%; Pred. No. 1.2e-11;
RESULT 829
ID ABG00258 standard; protein; 893 AA.
DE Novel human diagnostic protein #249.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 13.4%; Score 242.5; DB 4; Length 893;
Best Local Similarity 26.4%; Pred. No. 1.4e-11;
RESULT 830
ID ABG00611 standard; protein; 893 AA.
DE Novel human diagnostic protein #602.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 13.4%; Score 242.5; DB 4; Length 893;
Best Local Similarity 26.4%; Pred. No. 1.4e-11;
RESULT 831
ID ABG31317 standard; protein; 2586 AA.
DE Human 5+3 corrected OCP protein.
PN WO200246364-A2.
PD 13-JUN-2002.
PA (QUAR-) QUARK BIOTECH INC.
Query Match 13.4%; Score 242; DB 5; Length 2586;
Best Local Similarity 27.0%; Pred. No. 6.6e-11;
RESULT 832
ID ABG32891 standard; protein; 2586 AA.
DE Human osteoclast protein (OCP) #1.
PN US2002086825-A1.
PD 04-JUL-2002.
PA (EINA/) EINAT P.
PA (SEGE/) SEGEV O.
PA (SKAL/) SKALITER R.
PA (FEIN/) FEINSTEIN E.
PA (FAER/) FAERMAN A.
Query Match 13.4%; Score 242; DB 5; Length 2586;
Best Local Similarity 27.0%; Pred. No. 6.6e-11;
RESULT 833
ID ADL02231 standard; protein; 2586 AA.
DE Human OCP protein #1.
PN US2004053301-A1.
PD 18-MAR-2004.
PA (QUAR-) QUARK BIOTECH INC.
Query Match 13.4%; Score 242; DB 8; Length 2586;
Best Local Similarity 27.0%; Pred. No. 6.6e-11;
RESULT 834
ID ADL02234 standard; protein; 2586 AA.
DE Human OCP protein #2.
PN US2004053301-A1.
PD 18-MAR-2004.
PA (QUAR-) QUARK BIOTECH INC.
Query Match 13.4%; Score 242; DB 8; Length 2586;
Best Local Similarity 27.0%; Pred. No. 6.6e-11;
RESULT 835
ID AAB47935 standard; protein; 2587 AA.
DE Human OCP.
PN US2002022026-A1.
PD 21-FEB-2002.
PA (EINA/) EINAT P.
PA (SEGE/) SEGEV O.
PA (SKAL/) SKALITER R.
PA (FEIN/) FEINSTEIN E.
PA (FAER/) FAERMAN A.
Query Match 13.4%; Score 242; DB 5; Length 2587;
Best Local Similarity 27.0%; Pred. No. 6.6e-11;

RESULT 836
ID ABG32896 standard; protein; 2587 AA.
DE Human osteoclast protein (OCP) #2.
PN US2002086825-A1.
PD 04-JUL-2002.
PA (EINAT/) EINAT P.
PA (SEGEV/) SEGEV O.
PA (SKAL/) SKALITER R.
PA (FEIN/) FEINSTEIN E.
PA (FAER/) FAERMAN A.
Query Match 13.4%; Score 242; DB 5; Length 2587;
Best Local Similarity 27.0%; Pred. No. 6.6e-11;
RESULT 837
ID ADL02236 standard; protein; 2587 AA.
DE Human OCP protein #3.
PN US2004053301-A1.
PD 18-MAR-2004.
PA (QUAR-) QUARK BIOTECH INC.
Query Match 13.4%; Score 242; DB 8; Length 2587;
Best Local Similarity 27.0%; Pred. No. 6.6e-11;
RESULT 838
ID ABG31323 standard; protein; 2589 AA.
DE Human OCP protein.
PN WO200246364-A2.
PD 13-JUN-2002.
PA (QUAR-) QUARK BIOTECH INC.
Query Match 13.4%; Score 242; DB 5; Length 2589;
Best Local Similarity 27.0%; Pred. No. 6.7e-11;
RESULT 839
ID ADL02244 standard; protein; 2589 AA.
DE Human OCP protein #5.
PN US2004053301-A1.
PD 18-MAR-2004.
PA (QUAR-) QUARK BIOTECH INC.
Query Match 13.4%; Score 242; DB 8; Length 2589;
Best Local Similarity 27.0%; Pred. No. 6.7e-11;
RESULT 840
ID AAR92256 standard; protein; 582 AA.
DE Neural cell adhesion molecule splice variant.
PN WO9604396-A1.
PD 15-FEB-1996.
PA (SYST-) SYSTEMIX INC.
Query Match 13.4%; Score 241.5; DB 2; Length 582;
Best Local Similarity 24.4%; Pred. No. 9.5e-12;
RESULT 841
ID AAR92255 standard; protein; 761 AA.
DE Neural cell adhesion molecule.
PN WO9604396-A1.
PD 15-FEB-1996.
PA (SYST-) SYSTEMIX INC.
Query Match 13.4%; Score 241.5; DB 2; Length 761;
Best Local Similarity 24.4%; Pred. No. 1.4e-11;
RESULT 842
ID ADI24547 standard; protein; 837 AA.
DE Human modifier of Chk1 (MCHK) protein SEQ ID NO:97.
PN WO2004004785-A1.
PD 15-JAN-2004.
PA (EXEL-) EXELIXIS INC.
Query Match 13.4%; Score 241.5; DB 8; Length 837;
Best Local Similarity 24.7%; Pred. No. 1.6e-11;
RESULT 843
ID ADJ76385 standard; protein; 1020 AA.
DE Marker gene related amino acid sequence SEQ ID NO:1637.
PN EPI394274-A2.
PD 03-MAR-2004.
PA (GENO-) GENOX RES INC.
Query Match 13.4%; Score 241.5; DB 8; Length 1020;
Best Local Similarity 24.3%; Pred. No. 2.1e-11;
RESULT 844
ID AEA55089 standard; protein; 1020 AA.
DE Mouse contactin 1 protein, SEQ ID NO: 65.
PN WO2005052182-A2.
PD 09-JUN-2005.

PA (YISS) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.
Query Match 13.4%; Score 241.5; DB 9; Length 1020;
Best Local Similarity 24.3%; Pred. No. 2.1e-11;
RESULT 845
ID AEA55056 standard; protein; 1020 AA.
DE Mouse contactin 1 precursor protein, SEQ ID NO: 32.
PN WO2005052182-A2.
PD 09-JUN-2005.
PA (YISS) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.
Query Match 13.4%; Score 241.5; DB 9; Length 1020;
Best Local Similarity 24.3%; Pred. No. 2.1e-11;
RESULT 846
ID ABG07536 standard; protein; 891 AA.
DE Novel human diagnostic protein #7527.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSEQ-) HYSEQ INC.
Query Match 13.3%; Score 241; DB 4; Length 891;
Best Local Similarity 45.7%; Pred. No. 1.9e-11;
RESULT 847
ID ABP69251 standard; protein; 2173 AA.
DE Human polypeptide SEQ ID NO 1298.
PN WO200270539-A2.
PD 12-SEP-2002.
PA (HYSEQ-) HYSEQ INC.
Query Match 13.3%; Score 241; DB 5; Length 2173;
Best Local Similarity 26.7%; Pred. No. 6.4e-11;
RESULT 848
ID ADV70215 standard; protein; 3707 AA.
DE Tumor-associated antigenic target polypeptide TAT457.
PN WO2004112829-A2.
PD 29-DEC-2004.
PA (GETH) GENENTECH INC.
Query Match 13.3%; Score 240; DB 9; Length 3707;
Best Local Similarity 27.0%; Pred. No. 1.6e-10;
RESULT 849
ID AAE00585 standard; protein; 793 AA.
DE Human nuclear cell adhesion molecule homologue, NCAM_c_1 protein.
PN WO200129215-A2.
PD 26-APR-2001.
PA (COMP-) COMPUGEN LTD.
Query Match 13.2%; Score 238.5; DB 4; Length 793;
Best Local Similarity 25.4%; Pred. No. 2.6e-11;
RESULT 850
ID AAE00584 standard; protein; 848 AA.
DE Human nuclear cell adhesion molecule homologue, NCAM_c_2 protein.
PN WO200129215-A2.
PD 26-APR-2001.
PA (COMP-) COMPUGEN LTD.
Query Match 13.2%; Score 238.5; DB 4; Length 848;
Best Local Similarity 25.4%; Pred. No. 2.9e-11;
RESULT 851
ID AAE00586 standard; protein; 891 AA.
DE Human nuclear cell adhesion molecule homologue, NCAM_d_2 protein.
PN WO200129215-A2.
PD 26-APR-2001.
PA (COMP-) COMPUGEN LTD.
Query Match 13.2%; Score 238.5; DB 4; Length 891;
Best Local Similarity 25.4%; Pred. No. 3.1e-11;
RESULT 852
ID AAE00583 standard; protein; 920 AA.
DE Human cell adhesion molecule homologue (CAM-H) protein #2.
PN WO200129215-A2.
PD 26-APR-2001.
PA (COMP-) COMPUGEN LTD.
Query Match 13.2%; Score 238.5; DB 4; Length 920;
Best Local Similarity 25.4%; Pred. No. 3.2e-11;
RESULT 853
ID AAE00582 standard; protein; 946 AA.
DE Human nuclear cell adhesion molecule homologue, NCAM_d_1 protein.
PN WO200129215-A2.
PD 26-APR-2001.
PA (COMP-) COMPUGEN LTD.

Query Match 13.2%; Score 238.5; DB 4; Length 946;
Best Local Similarity 25.4%; Pred. No. 3.4e-11;
RESULT 854
ID AAB00581 standard; protein; 1018 AA.
DE Human cell adhesion molecule homologue (CAM-H) protein #1.
PN WO200129215-A2.
PD 26-APR-2001.
PA (COMP-) COMPUGEN LTD.
Query Match 13.2%; Score 238.5; DB 4; Length 1018;
Best Local Similarity 25.4%; Pred. No. 3.7e-11;
RESULT 855
ID AAW05161 standard; protein; 73 AA.
DE Human LAMP residues 46-118.
PN WO9630052-A1.
PD 03-OCT-1996.
PA (UMDN-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.
Query Match 13.1%; Score 237; DB 2; Length 73;
Best Local Similarity 58.3%; Pred. No. 1.4e-12;
RESULT 856
ID AAW05162 standard; protein; 73 AA.
DE Rat LAMP residues 46-118.
PN WO9630052-A1.
PD 03-OCT-1996.
PA (UMDN-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.
Query Match 13.1%; Score 237; DB 2; Length 73;
Best Local Similarity 58.3%; Pred. No. 1.4e-12;
RESULT 857
ID ADR09877 standard; protein; 632 AA.
DE Human protein useful for treating neurological disease Seq 3383.
PN EP147413-A2.
PD 18-AUG-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 13.0%; Score 235.5; DB 8; Length 632;
Best Local Similarity 26.9%; Pred. No. 3.5e-11;
RESULT 858
ID ADH71818 standard; protein; 967 AA.
DE Human protein of the invention NOV29y SEQ ID NO:714.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 13.0%; Score 235.5; DB 8; Length 967;
Best Local Similarity 27.1%; Pred. No. 6.3e-11;
RESULT 859
ID ADS10576 standard; protein; 2428 AA.
DE Human therapeutic protein - SEQ ID 813.
PN WO2004080148-A2.
PD 23-SEP-2004.
PA (NUVE-) NUVELO INC.
Query Match 13.0%; Score 235.5; DB 8; Length 2428;
Best Local Similarity 26.9%; Pred. No. 2.2e-10;
RESULT 860
ID ADL02252 standard; protein; 2623 AA.
DE Human OCP protein #7.
PN US2004053301-A1.
PD 18-MAR-2004.
PA (QUAR-) QUARK BIOTECH INC.
Query Match 13.0%; Score 235.5; DB 8; Length 2623;
Best Local Similarity 26.9%; Pred. No. 2.5e-10;
RESULT 861
ID ADS10577 standard; protein; 2623 AA.
DE Human therapeutic protein - SEQ ID 814.
PN WO2004080148-A2.
PD 23-SEP-2004.
PA (NUVE-) NUVELO INC.
Query Match 13.0%; Score 235.5; DB 8; Length 2623;
Best Local Similarity 26.9%; Pred. No. 2.5e-10;
RESULT 862
ID ADN24073 standard; protein; 662 AA.
DE Bacterial polypeptide #6726.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.

PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 13.0%; Score 235; DB 8; Length 662;
Best Local Similarity 25.5%; Pred. No. 4.1e-11;
RESULT 863
ID ADD47171 standard; protein; 1040 AA.
DE Rat Protein AAM42201, SEQ ID NO 12864.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 13.0%; Score 234.5; DB 7; Length 1040;
Best Local Similarity 25.8%; Pred. No. 8.5e-11;
RESULT 864
ID ADR67266 standard; protein; 1100 AA.
DE Human bladder cancer associated amino acid sequence.
PN WO2004076613-A2.
PD 10-SEP-2004.
PA (HERR/) HERR A.
PA (HINZ/) HINZMANN B.
PA (DAHL/) DAHL E.
PA (STAU/) STAUB E.
PA (PILA/) PILARSKY C.
PA (SPEC/) SPECHT T.
Query Match 12.9%; Score 233.5; DB 8; Length 1100;
Best Local Similarity 24.9%; Pred. No. 1.1e-10;
RESULT 865
ID ADH71816 standard; protein; 967 AA.
DE Human protein of the invention NOV29x SEQ ID NO:712.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 12.9%; Score 232.5; DB 8; Length 967;
Best Local Similarity 26.8%; Pred. No. 1.1e-10;
RESULT 866
ID ADN23691 standard; protein; 2783 AA.
DE Bacterial polypeptide #6344.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 12.9%; Score 232.5; DB 8; Length 2783;
Best Local Similarity 23.5%; Pred. No. 4.8e-10;
RESULT 867
ID ABG69614 standard; protein; 2401 AA.
DE Human NOV12a protein.
PN WO200250277-A2.
PD 27-JUN-2002.
PA (CURA-) CURAGEN CORP.
Query Match 12.8%; Score 232; DB 5; Length 2401;
Best Local Similarity 26.9%; Pred. No. 4.4e-10;
RESULT 868
ID ABG69619 standard; protein; 2447 AA.
DE Human NOV12f protein.
PN WO200250277-A2.
PD 27-JUN-2002.
PA (CURA-) CURAGEN CORP.
Query Match 12.8%; Score 232; DB 5; Length 2447;
Best Local Similarity 26.9%; Pred. No. 4.5e-10;
RESULT 869
ID ADJ83065 standard; protein; 2591 AA.
DE Human NOVX NOV12f protein.
PN US2003170630-A1.
PD 11-SEP-2003.
PA (ALSO/) ALSOBROOK J P.
PA (TCHE/) TCHERNEV V T.
PA (LIUX/) LIU X.
PA (SPYT/) SPYTEK K A.
PA (ZERH/) ZERHUSEN B D.

PA (PATT/) PATTURAJAN M.
 PA (LEPL/) LEPLY D M.
 PA (BURG/) BURGESS C E.
 PA (SHIM/) SHIMKETS R A.
 PA (GROS/) GROSSE W M.
 PA (SZEK/) SZEKERES E S.
 PA (VERN/) VERNET C A M.
 PA (LILL/) LI L.
 PA (CASM/) CASMAN S J.
 PA (BOLD/) BOLDOG F L.
 PA (GORM/) GORMAN L.
 PA (GANG/) GANGOLLI E A.
 PA (FERN/) FERNANDES E R.
 PA (RIEG/) RIEGER D K.
 PA (EDIN/) EDINGER S R.
 PA (GUNT/) GUNTHER E.
 PA (MILL/) MILLET I.
 PA (SCIO/) SCIORE P.
 PA (ELLE/) ELLERMAN K.
 PA (MACD/) MACDOUGALL J R.
 PA (SMIT/) SMITHSON G.
 Query Match 12.8%; Score 232; DB 7; Length 2591;
 Best Local Similarity 26.9%; Pred. No. 4.9e-10;
 RESULT 870
 ID ADH71822 standard; protein; 2591 AA.
 DE Human protein of the invention NOV29aa SEQ ID NO:718.
 PN WO2003102155-A2.
 PD 11-DEC-2003.
 PA (CURA-) CURAGEN CORP.
 Query Match 12.8%; Score 232; DB 8; Length 2591;
 Best Local Similarity 26.9%; Pred. No. 4.9e-10;
 RESULT 871
 ID ADH71820 standard; protein; 2602 AA.
 DE Human protein of the invention NOV29z SEQ ID NO:716.
 PN WO2003102155-A2.
 PD 11-DEC-2003.
 PA (CURA-) CURAGEN CORP.
 Query Match 12.8%; Score 232; DB 8; Length 2602;
 Best Local Similarity 26.9%; Pred. No. 4.9e-10;
 RESULT 872
 ID ADJ83055 standard; protein; 2617 AA.
 DE Human NOVX NOV12a protein.
 PN US2003170630-A1.
 PD 11-SEP-2003.
 PA (ALSO/) ALSOBROOK J P.
 PA (TCHE/) TCHERNEV V T.
 PA (LIUX/) LIU X.
 PA (SPYT/) SPYTEK K A.
 PA (ZERH/) ZERHUSEN B D.
 PA (PATT/) PATTURAJAN M.
 PA (LEPL/) LEPLY D M.
 PA (BURG/) BURGESS C E.
 PA (SHIM/) SHIMKETS R A.
 PA (GROS/) GROSSE W M.
 PA (SZEK/) SZEKERES E S.
 PA (VERN/) VERNET C A M.
 PA (LILL/) LI L.
 PA (CASM/) CASMAN S J.
 PA (BOLD/) BOLDOG F L.
 PA (GORM/) GORMAN L.
 PA (GANG/) GANGOLLI E A.
 PA (FERN/) FERNANDES E R.
 PA (RIEG/) RIEGER D K.
 PA (EDIN/) EDINGER S R.
 PA (GUNT/) GUNTHER E.
 PA (SCIO/) SCIORE P.
 PA (ELLE/) ELLERMAN K.
 PA (MACD/) MACDOUGALL J R.
 PA (SMIT/) SMITHSON G.
 Query Match 12.8%; Score 232; DB 7; Length 2617;
 Best Local Similarity 26.9%; Pred. No. 4.9e-10;
 RESULT 873
 ID ADH71842 standard; protein; 2617 AA.
 DE Human protein of the invention NOV29ak SEQ ID NO:738.
 PN WO2003102155-A2.
 PD 11-DEC-2003.
 PA (CURA-) CURAGEN CORP.
 Query Match 12.8%; Score 232; DB 8; Length 2617;
 Best Local Similarity 26.9%; Pred. No. 4.9e-10;
 RESULT 874
 ID ADH71852 standard; protein; 2617 AA.
 DE Human protein of the invention NOV29ap SEQ ID NO:748.
 PN WO2003102155-A2.
 PD 11-DEC-2003.
 PA (CURA-) CURAGEN CORP.
 Query Match 12.8%; Score 232; DB 8; Length 2617;
 Best Local Similarity 26.9%; Pred. No. 4.9e-10;
 RESULT 875
 ID ADH71838 standard; protein; 2617 AA.
 DE Human protein of the invention NOV29ai SEQ ID NO:734.
 PN WO2003102155-A2.
 PD 11-DEC-2003.
 PA (CURA-) CURAGEN CORP.
 Query Match 12.8%; Score 232; DB 8; Length 2617;
 Best Local Similarity 26.9%; Pred. No. 4.9e-10;
 RESULT 876
 ID ADH71770 standard; protein; 2617 AA.
 DE Human protein of the invention NOV29a SEQ ID NO:666.
 PN WO2003102155-A2.
 PD 11-DEC-2003.
 PA (CURA-) CURAGEN CORP.
 Query Match 12.8%; Score 232; DB 8; Length 2617;
 Best Local Similarity 26.9%; Pred. No. 4.9e-10;
 RESULT 877
 ID ADH71836 standard; protein; 2617 AA.
 DE Human protein of the invention NOV29ah SEQ ID NO:732.
 PN WO2003102155-A2.
 PD 11-DEC-2003.
 PA (CURA-) CURAGEN CORP.
 Query Match 12.8%; Score 232; DB 8; Length 2617;
 Best Local Similarity 26.9%; Pred. No. 4.9e-10;
 RESULT 878
 ID ADH71840 standard; protein; 2617 AA.
 DE Human protein of the invention NOV29aj SEQ ID NO:736.
 PN WO2003102155-A2.
 PD 11-DEC-2003.
 PA (CURA-) CURAGEN CORP.
 Query Match 12.8%; Score 232; DB 8; Length 2617;
 Best Local Similarity 26.9%; Pred. No. 4.9e-10;
 RESULT 879
 ID ADH71844 standard; protein; 2617 AA.
 DE Human protein of the invention NOV29al SEQ ID NO:740.
 PN WO2003102155-A2.
 PD 11-DEC-2003.
 PA (CURA-) CURAGEN CORP.
 Query Match 12.8%; Score 232; DB 8; Length 2617;
 Best Local Similarity 26.9%; Pred. No. 4.9e-10;
 RESULT 880
 ID ADH71846 standard; protein; 2617 AA.
 DE Human protein of the invention NOV29am SEQ ID NO:742.
 PN WO2003102155-A2.
 PD 11-DEC-2003.
 PA (CURA-) CURAGEN CORP.
 Query Match 12.8%; Score 232; DB 8; Length 2617;
 Best Local Similarity 26.9%; Pred. No. 4.9e-10;
 RESULT 881
 ID ADH71850 standard; protein; 2617 AA.
 DE Human protein of the invention NOV29ao SEQ ID NO:746.
 PN WO2003102155-A2.
 PD 11-DEC-2003.
 PA (CURA-) CURAGEN CORP.
 Query Match 12.8%; Score 232; DB 8; Length 2617;
 Best Local Similarity 26.9%; Pred. No. 4.9e-10;
 RESULT 882
 ID ADH71854 standard; protein; 2617 AA.

DE Human protein of the invention NOV29aq SEQ ID NO:750.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 12.8%; Score 232; DB 8; Length 2617;
Best Local Similarity 26.9%; Pred. No. 4.9e-10;
RESULT 883
ID ADH71848 standard; protein; 2617 AA.
DE Human protein of the invention NOV29an SEQ ID NO:744.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 12.8%; Score 232; DB 8; Length 2617;
Best Local Similarity 26.9%; Pred. No. 4.9e-10;
RESULT 884
ID AB07377 standard; protein; 3931 AA.
DE Human protein NOV9.
PN WO200285922-A2.
PD 31-OCT-2002.
PA (CURA-) CURAGEN CORP.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 12.8%; Score 232; DB 6; Length 3931;
Best Local Similarity 28.3%; Pred. No. 8.6e-10;
RESULT 885
ID AAW29667 standard; protein; 1028 AA.
DE Homo sapiens DL185_1 clone secreted protein.
PN WO9830693-A2.
PD 16-JUL-1998.
PA (GEMV-) GENETICS INST INC.
Query Match 12.8%; Score 231; DB 2; Length 1028;
Best Local Similarity 26.7%; Pred. No. 1.7e-10;
RESULT 886
ID ADP67247 standard; protein; 1028 AA.
DE Human NB-3 protein.
PN WO2004052389-A2.
PD 24-JUN-2004.
PA (SIGE-) SINGAPORE GEN HOSPITAL PTE LTD.
PA (FORR-) FORREST G R.
Query Match 12.8%; Score 231; DB 8; Length 1028;
Best Local Similarity 26.7%; Pred. No. 1.7e-10;
RESULT 887
ID ADG39786 standard; protein; 3931 AA.
DE Human novel protein NOV9.
PN US2003203843-A1.
PD 30-OCT-2003.
PA (PENA/) PENA C E A.
PA (GUOX/) GUO X.
PA (SHIM/) SHIMKETS R A.
PA (PADI/) PADIGARU M.
PA (KEKU/) KEKUDA R.
PA (SPYT/) SPYTEK K A.
PA (MEHR/) MEHRABAN F.
PA (TOPP/) TOPPER J N.
PA (MALY/) MALYANKAR U M.
PA (WASS/) WASSERMAN S M.
PA (EDIN/) EDINGER S R.
PA (SMIT/) SMITHSON G.
PA (GUNT/) GUNTHER E.
PA (KOMU/) KOMUVES L.
Query Match 12.8%; Score 231; DB 7; Length 3931;
Best Local Similarity 28.3%; Pred. No. 1e-09;
RESULT 888
ID AEC74506 standard; protein; 861 AA.
DE Muscle-specific kinase (MUSK) SEQ ID NO 2.
PN WO2005084184-A2.
PD 15-SEP-2005.
PA (MOUN-) MOUNT SINAI SCHOOL MEDICINE.
PA (KLEI/) KLEIM J.
Query Match 12.8%; Score 230.5; DB 9; Length 861;
Best Local Similarity 25.2%; Pred. No. 1.4e-10;
RESULT 889
ID AAW26507 standard; protein; 868 AA.
DE Rat Dmk receptor.
PN US5656473-A.
PD 12-AUG-1997.
PA (REGE-) REGENERON PHARM INC.
Query Match 12.8%; Score 230.5; DB 2; Length 868;
Best Local Similarity 25.2%; Pred. No. 1.5e-10;
RESULT 890
ID AAW26610 standard; protein; 868 AA.
DE Rat muscle-specific kinase (MUSK).
PN WO9721811-A2.
PD 19-JUN-1997.
PA (REGE-) REGENERON PHARM INC.
Query Match 12.8%; Score 230.5; DB 2; Length 868;
Best Local Similarity 25.2%; Pred. No. 1.5e-10;
RESULT 891
ID ADH71830 standard; protein; 961 AA.
DE Human protein of the invention NOV29ae SEQ ID NO:726.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 12.8%; Score 230.5; DB 8; Length 961;
Best Local Similarity 27.2%; Pred. No. 1.7e-10;
RESULT 892
ID ADH71832 standard; protein; 961 AA.
DE Human protein of the invention NOV29af SEQ ID NO:728.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 12.8%; Score 230.5; DB 8; Length 961;
Best Local Similarity 27.2%; Pred. No. 1.7e-10;
RESULT 893
ID AB084727 standard; protein; 1040 AA.
DE Mouse cancer-associated protein MP22-025.1.
PN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 12.8%; Score 230.5; DB 8; Length 1040;
Best Local Similarity 25.0%; Pred. No. 1.9e-10;
RESULT 894
ID AB08469 standard; protein; 3475 AA.
DE Human cancer-associated protein HPI3-036.1.
PN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 12.8%; Score 230.5; DB 8; Length 3475;
Best Local Similarity 24.3%; Pred. No. 9.8e-10;
RESULT 895
ID ADG39842 standard; protein; 1928 AA.
DE Protein similar to human NOV9 #3.
PN US2003203843-A1.
PD 30-OCT-2003.
PA (PENA/) PENA C E A.
PA (GUOX/) GUO X.
PA (SHIM/) SHIMKETS R A.
PA (PADI/) PADIGARU M.
PA (KEKU/) KEKUDA R.
PA (SPYT/) SPYTEK K A.
PA (MEHR/) MEHRABAN F.
PA (TOPP/) TOPPER J N.
PA (MALY/) MALYANKAR U M.
PA (WASS/) WASSERMAN S M.
PA (EDIN/) EDINGER S R.
PA (SMIT/) SMITHSON G.
PA (GUNT/) GUNTHER E.
PA (KOMU/) KOMUVES L.
Query Match 12.7%; Score 230; DB 7; Length 1928;
Best Local Similarity 22.9%; Pred. No. 4.8e-10;
RESULT 896
ID ADG39843 standard; protein; 1951 AA.
DE Protein similar to human NOV9 #4.
PN US2003203843-A1.
PD 30-OCT-2003.
PA (PENA/) PENA C E A.
PA (GUOX/) GUO X.

PA (SHIM/) SHIMKETS R A.
PA (PADI/) PADIGARU M.
PA (KEKU/) KEKUDA R.
PA (SPYT/) SPYTEK K A.
PA (MEHR/) MEHRABAN F.
PA (TOPP/) TOPPER J N.
PA (MALY/) MALYANKAR U M.
PA (WASS/) WASSERMAN S M.
PA (EDIN/) EDINGER S R.
PA (SMIT/) SMITHSON G.
PA (GUNT/) GUNTHER E.
PA (KOWU/) KOMOVES L.
Query Match 12.7%; Score 230; DB 7; Length 1951;
Best Local Similarity 22.9%; Pred. No. 4.9e-10;
RESULT 897
ID AAV53667 standard; protein; 3117 AA.
DE Sequence gi/3328186 from an alignment with protein 608.
PN WO9960164-A1.
PD 25-NOV-1999.
PA (QUAR-) QUARK BIOTECH INC.
Query Match 12.7%; Score 230; DB 3; Length 3117;
Best Local Similarity 22.9%; Pred. No. 9.3e-10;
RESULT 898
ID AAB31899 standard; protein; 4393 AA.
DE Amino acid sequence of a human protein.
PN WO200105422-A2.
PD 25-JAN-2001.
PA (INNR-) BIOMERIEUX STELHYS.
Query Match 12.7%; Score 230; DB 4; Length 4393;
Best Local Similarity 26.0%; Pred. No. 1.5e-09;
RESULT 899
ID ADL35758 standard; protein; 4393 AA.
DE Human perlecan (heparan sulphate proteoglycan 2; HSPG2) protein.
PN WO2004019893-A2.
PD 11-MAR-2004.
PA (RIGE-) RIGEL PHARM INC.
Query Match 12.7%; Score 230; DB 8; Length 4393;
Best Local Similarity 26.0%; Pred. No. 1.5e-09;
RESULT 900
ID ADQ39442 standard; protein; 4393 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1105.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match 12.7%; Score 230; DB 8; Length 4393;
Best Local Similarity 26.0%; Pred. No. 1.5e-09;
RESULT 901
ID AED74327 standard; protein; 4419 AA.
DE Human placental protein SEQ ID NO:1155.
PN US2005255114-A1.
PD 17-NOV-2005.
PA (NUVE-) NUVELO INC.
Query Match 12.7%; Score 230; DB 9; Length 4419;
Best Local Similarity 26.0%; Pred. No. 1.5e-09;
RESULT 902
ID ABG23265 standard; protein; 4436 AA.
DE Novel human diagnostic protein #23256.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSEQ-) HYSEQ INC.
Query Match 12.7%; Score 230; DB 4; Length 4436;
Best Local Similarity 26.0%; Pred. No. 1.5e-09;
RESULT 903
ID ADL16585 standard; protein; 849 AA.
DE Human 282PIG3 polypeptide #35.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Query Match 12.7%; Score 229.5; DB 8; Length 849;
Best Local Similarity 25.6%; Pred. No. 1.7e-10;
RESULT 904
ID ADL16586 standard; protein; 851 AA.
DE Human 282PIG3 polypeptide #36.

PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Query Match 12.7%; Score 229.5; DB 8; Length 851;
Best Local Similarity 25.6%; Pred. No. 1.7e-10;
RESULT 905
ID AAM26506 standard; protein; 869 AA.
DE Human Dmk receptor.
PN US5656473-A.
PD 12-AUG-1997.
PA (REGE-) REGENERON PHARM INC.
Query Match 12.7%; Score 229.5; DB 2; Length 869;
Best Local Similarity 26.4%; Pred. No. 1.8e-10;
RESULT 906
ID AAW26611 standard; protein; 869 AA.
DE Human muscle-specific kinase (MUSK).
PN WO9721811-A2.
PD 19-JUN-1997.
PA (REGE-) REGENERON PHARM INC.
Query Match 12.7%; Score 229.5; DB 2; Length 869;
Best Local Similarity 26.4%; Pred. No. 1.8e-10;
RESULT 907
ID ADQ89844 standard; protein; 869 AA.
DE Antagonist of cell cycle progression polypeptide #137.
PN WO2004063362-A2.
PD 29-JUL-2004.
PA (CYCL-) CYCLACEL LTD.
Query Match 12.7%; Score 229.5; DB 8; Length 869;
Best Local Similarity 26.4%; Pred. No. 1.8e-10;
RESULT 908
ID ADL16446 standard; protein; 893 AA.
DE Human 282PIG3 polypeptide #12.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Query Match 12.7%; Score 229.5; DB 8; Length 893;
Best Local Similarity 25.6%; Pred. No. 1.9e-10;
RESULT 909
ID ADL16584 standard; protein; 893 AA.
DE Human 282PIG3 polypeptide #34.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Query Match 12.7%; Score 229.5; DB 8; Length 893;
Best Local Similarity 25.6%; Pred. No. 1.9e-10;
RESULT 910
ID ADL16625 standard; protein; 893 AA.
DE Human 282PIG3 polypeptide #57.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Query Match 12.7%; Score 229.5; DB 8; Length 893;
Best Local Similarity 25.6%; Pred. No. 1.9e-10;
RESULT 911
ID ADL16431 standard; protein; 893 AA.
DE Human 282PIG3 polypeptide #3.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Query Match 12.7%; Score 229.5; DB 8; Length 893;
Best Local Similarity 25.6%; Pred. No. 1.9e-10;
RESULT 912
ID ADL16626 standard; protein; 1117 AA.
DE Human 282PIG3 polypeptide #58.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Query Match 12.7%; Score 229.5; DB 8; Length 1117;
Best Local Similarity 25.6%; Pred. No. 2.5e-10;
RESULT 913
ID ADL16590 standard; protein; 1117 AA.
DE Human 282PIG3 polypeptide #37.
PN WO2004016734-A2.

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PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Query Match 12.7%; Score 229.5; DB 8; Length 1117;
Best Local Similarity 25.6%; Pred. No. 2.5e-10;
RESULT 914
ID ADL16447 standard; protein; 1117 AA.
DE Human 282PiG3 polypeptide #13.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Query Match 12.7%; Score 229.5; DB 8; Length 1117;
Best Local Similarity 25.6%; Pred. No. 2.5e-10;
RESULT 915
ID ADL16433 standard; protein; 1117 AA.
DE Human 282PiG3 polypeptide #4.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Query Match 12.7%; Score 229.5; DB 8; Length 1117;
Best Local Similarity 25.6%; Pred. No. 2.5e-10;
RESULT 916
ID ADL16592 standard; protein; 1117 AA.
DE Human 282PiG3 polypeptide #39.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Query Match 12.7%; Score 229.5; DB 8; Length 1117;
Best Local Similarity 25.6%; Pred. No. 2.5e-10;
RESULT 917
ID A8M83685 standard; protein; 1171 AA.
DE Human diagnostic and therapeutic pprotein SEQ ID NO.3934.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 12.7%; Score 229.5; DB 8; Length 1171;
Best Local Similarity 25.6%; Pred. No. 2.7e-10;
RESULT 918
ID ADL16604 standard; protein; 1183 AA.
DE Human 282PiG3 polypeptide #45.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Query Match 12.7%; Score 229.5; DB 8; Length 1183;
Best Local Similarity 25.6%; Pred. No. 2.7e-10;
RESULT 919
ID ADL16628 standard; protein; 1183 AA.
DE Human 282PiG3 polypeptide #60.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Query Match 12.7%; Score 229.5; DB 8; Length 1183;
Best Local Similarity 25.6%; Pred. No. 2.7e-10;
RESULT 920
ID ADL16449 standard; protein; 1183 AA.
DE Human 282PiG3 polypeptide #15.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Query Match 12.7%; Score 229.5; DB 8; Length 1183;
Best Local Similarity 25.6%; Pred. No. 2.7e-10;
RESULT 921
ID ADL16602 standard; protein; 1183 AA.
DE Human 282PiG3 polypeptide #43.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Query Match 12.7%; Score 229.5; DB 8; Length 1183;
Best Local Similarity 25.6%; Pred. No. 2.7e-10;
RESULT 922
ID ADL16437 standard; protein; 1183 AA.
DE Human 282PiG3 polypeptide #6.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Query Match 12.7%; Score 229.5; DB 8; Length 1224;
Best Local Similarity 25.6%; Pred. No. 2.9e-10;
RESULT 923
ID ADL16448 standard; protein; 1208 AA.
DE Human 282PiG3 polypeptide #14.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Query Match 12.7%; Score 229.5; DB 8; Length 1208;
Best Local Similarity 25.6%; Pred. No. 2.8e-10;
RESULT 924
ID ADL16596 standard; protein; 1208 AA.
DE Human 282PiG3 polypeptide #40.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Query Match 12.7%; Score 229.5; DB 8; Length 1208;
Best Local Similarity 25.6%; Pred. No. 2.8e-10;
RESULT 925
ID ADL16435 standard; protein; 1208 AA.
DE Human 282PiG3 polypeptide #5.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Query Match 12.7%; Score 229.5; DB 8; Length 1208;
Best Local Similarity 25.6%; Pred. No. 2.8e-10;
RESULT 926
ID ADL16627 standard; protein; 1208 AA.
DE Human 282PiG3 polypeptide #59.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Query Match 12.7%; Score 229.5; DB 8; Length 1208;
Best Local Similarity 25.6%; Pred. No. 2.8e-10;
RESULT 927
ID ADL16598 standard; protein; 1208 AA.
DE Human 282PiG3 polypeptide #42.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Query Match 12.7%; Score 229.5; DB 8; Length 1208;
Best Local Similarity 25.6%; Pred. No. 2.8e-10;
RESULT 928
ID ADJ69602 standard; protein; 1224 AA.
DE Human heat mitochondrial protein as-a therapeutic target SeqID1408.
PN WO2003087768-A2.
PD 23-OCT-2003.
PA (MITO-) MITOKOR.
PA (BUCK-) BUCK INST AGE RES.
Query Match 12.7%; Score 229.5; DB 7; Length 1224;
Best Local Similarity 25.6%; Pred. No. 2.9e-10;
RESULT 929
ID ADL16443 standard; protein; 1224 AA.
DE Human 282PiG3 polypeptide #9.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Query Match 12.7%; Score 229.5; DB 8; Length 1224;
Best Local Similarity 25.6%; Pred. No. 2.9e-10;
RESULT 930
ID ADL16597 standard; protein; 1224 AA.
DE Human 282PiG3 polypeptide #41.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Query Match 12.7%; Score 229.5; DB 8; Length 1224;
Best Local Similarity 25.6%; Pred. No. 2.9e-10;
RESULT 931
ID ADL16621 standard; protein; 1224 AA.
DE Human 282PiG3 polypeptide #53.
PN WO2004016734-A2.
PD 26-FEB-2004.
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PA (AGEN-) AGENSYS INC.	Query Match	12.7%;	Score 229.5;	DB 8;	Length 1224;
Best Local Similarity	25.6%;	Pred. No. 2.9e-10;			
RESULT 932					
ID ADL16452 standard; protein; 1224 AA.					
DE Human 282PIG3 polypeptide #18.					
PN WO2004016734-A2.					
PD 26-FEB-2004.					
PA (AGEN-) AGENSYS INC.	Query Match	12.7%;	Score 229.5;	DB 8;	Length 1224;
Best Local Similarity	25.6%;	Pred. No. 2.9e-10;			
RESULT 933					
ID ADL16623 standard; protein; 1224 AA.					
DE Human 282PIG3 polypeptide #55.					
PN WO2004016734-A2.					
PD 26-FEB-2004.					
PA (AGEN-) AGENSYS INC.	Query Match	12.7%;	Score 229.5;	DB 8;	Length 1224;
Best Local Similarity	25.8%;	Pred. No. 2.9e-10;			
RESULT 934					
ID ADL16579 standard; protein; 1224 AA.					
DE Human 282PIG3 polypeptide #32.					
PN WO2004016734-A2.					
PD 26-FEB-2004.					
PA (AGEN-) AGENSYS INC.	Query Match	12.7%;	Score 229.5;	DB 8;	Length 1224;
Best Local Similarity	25.6%;	Pred. No. 2.9e-10;			
RESULT 935					
ID ADL16427 standard; protein; 1224 AA.					
DE Human 282PIG3 polypeptide #1.					
PN WO2004016734-A2.					
PD 26-FEB-2004.					
PA (AGEN-) AGENSYS INC.	Query Match	12.7%;	Score 229.5;	DB 8;	Length 1224;
Best Local Similarity	25.6%;	Pred. No. 2.9e-10;			
RESULT 936					
ID ADL16455 standard; protein; 1224 AA.					
DE Human 282PIG3 polypeptide #21.					
PN WO2004016734-A2.					
PD 26-FEB-2004.					
PA (AGEN-) AGENSYS INC.	Query Match	12.7%;	Score 229.5;	DB 8;	Length 1224;
Best Local Similarity	25.6%;	Pred. No. 2.9e-10;			
RESULT 937					
ID ADL16457 standard; protein; 1224 AA.					
DE Human 282PIG3 polypeptide #23.					
PN WO2004016734-A2.					
PD 26-FEB-2004.					
PA (AGEN-) AGENSYS INC.	Query Match	12.7%;	Score 229.5;	DB 8;	Length 1224;
Best Local Similarity	25.6%;	Pred. No. 2.9e-10;			
RESULT 938					
ID ADL16591 standard; protein; 1224 AA.					
DE Human 282PIG3 polypeptide #38.					
PN WO2004016734-A2.					
PD 26-FEB-2004.					
PA (AGEN-) AGENSYS INC.	Query Match	12.7%;	Score 229.5;	DB 8;	Length 1224;
Best Local Similarity	25.6%;	Pred. No. 2.9e-10;			
RESULT 939					
ID ADL16620 standard; protein; 1224 AA.					
DE Human 282PIG3 polypeptide #52.					
PN WO2004016734-A2.					
PD 26-FEB-2004.					
PA (AGEN-) AGENSYS INC.	Query Match	12.7%;	Score 229.5;	DB 8;	Length 1224;
Best Local Similarity	25.8%;	Pred. No. 2.9e-10;			
RESULT 940					
ID ADL16456 standard; protein; 1224 AA.					
DE Human 282PIG3 polypeptide #22.					
PN WO2004016734-A2.					
PD 26-FEB-2004.					
PA (AGEN-) AGENSYS INC.	Query Match	12.7%;	Score 229.5;	DB 8;	Length 1224;
Best Local Similarity	25.6%;	Pred. No. 2.9e-10;			
RESULT 941					
ID ADL16615 standard; protein; 1224 AA.					
DE Human 282PIG3 polypeptide #50.					
PN WO2004016734-A2.					
PD 26-FEB-2004.					
PA (AGEN-) AGENSYS INC.	Query Match	12.7%;	Score 229.5;	DB 8;	Length 1224;
Best Local Similarity	25.6%;	Pred. No. 2.9e-10;			
RESULT 942					
ID ADL16622 standard; protein; 1224 AA.					
DE Human 282PIG3 polypeptide #54.					
PN WO2004016734-A2.					
PD 26-FEB-2004.					
PA (AGEN-) AGENSYS INC.	Query Match	12.7%;	Score 229.5;	DB 8;	Length 1224;
Best Local Similarity	25.6%;	Pred. No. 2.9e-10;			
RESULT 943					
ID ADL16444 standard; protein; 1224 AA.					
DE Human 282PIG3 polypeptide #10.					
PN WO2004016734-A2.					
PD 26-FEB-2004.					
PA (AGEN-) AGENSYS INC.	Query Match	12.7%;			

Best Local Similarity 25.6%; Pred. No. 2.9e-10;
RESULT 950
ID ADI6609 standard; protein; 1224 AA.
DE Human 282P1G3 polypeptide #47.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Query Match 12.7%; Score 229.5; DB 8; Length 1224;
Best Local Similarity 25.6%; Pred. No. 2.9e-10;
RESULT 951
ID ADQ39441 standard; protein; 3588 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1104.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match 12.7%; Score 229; DB 8; Length 3588;
Best Local Similarity 26.0%; Pred. No. 1.4e-09;
RESULT 952
ID ADQ39440 standard; protein; 4346 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1103.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match 12.7%; Score 229; DB 8; Length 4346;
Best Local Similarity 26.0%; Pred. No. 1.8e-09;
RESULT 953
ID ADQ39439 standard; protein; 4347 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1102.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match 12.7%; Score 229; DB 8; Length 4347;
Best Local Similarity 26.0%; Pred. No. 1.8e-09;
RESULT 954
ID ADJ69461 standard; protein; 4370 AA.
DE Human heat mitochondrial protein as a therapeutic target SeqID1267.
PN WO2003087768-A2.
PD 23-OCT-2003.
PA (MITO-) MITOKOR.
PA (BUCK-) BUCK INST AGE RES.
Query Match 12.7%; Score 229; DB 7; Length 4370;
Best Local Similarity 26.0%; Pred. No. 1.8e-09;
RESULT 955
ID ABG16336 standard; protein; 1483 AA.
DE Novel human diagnostic protein #16327.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 12.6%; Score 228; DB 4; Length 1483;
Best Local Similarity 24.1%; Pred. No. 5e-10;
RESULT 956
ID ADV97842 standard; protein; 8523 AA.
DE Murine protein kinase enzyme Seq 162.
PN WO200500200-A2.
PD 06-JAN-2005.
PA (SUGE-) SUGEN INC.
Query Match 12.6%; Score 227.5; DB 9; Length 8523;
Best Local Similarity 25.6%; Pred. No. 6e-09;
RESULT 957
ID ACE80586 standard; protein; 1189 AA.
DE Human ovarian cancer marker fragment SEQ ID NO 953.
PN WO2005116850-A2.
PD 08-DEC-2005.
PA (COMP-) COMPUGEN LTD.
Query Match 12.6%; Score 227; DB 10; Length 1189;
Best Local Similarity 25.7%; Pred. No. 4.5e-10;
RESULT 958
ID AEF71405 standard; protein; 1189 AA.
DE Human immunoglobulin superfamily, member 9, protein SEQ ID NO:56.
PN WO2006014999-A2.
PD 09-FEB-2006.
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
Query Match 12.6%; Score 227; DB 10; Length 1189;
Best Local Similarity 25.7%; Pred. No. 4.5e-10;
RESULT 959
ID AEF57722 standard; protein; 717 AA.
DE Human secreted protein PRO19837/UNQ5931.
PN WO2005112619-A2.
PD 01-DEC-2005.
PA (GETH-) GENENTECH INC.
PA (LEXI-) LEXICON GENETICS INC.
Query Match 12.5%; Score 226; DB 9; Length 717;
Best Local Similarity 24.8%; Pred. No. 2.8e-10;
RESULT 960
ID ABE80587 standard; protein; 717 AA.
DE Human ovarian cancer marker fragment SEQ ID NO 954.
PN WO2005116850-A2.
PD 08-DEC-2005.
PA (COMP-) COMPUGEN LTD.
Query Match 12.5%; Score 226; DB 10; Length 717;
Best Local Similarity 24.8%; Pred. No. 2.8e-10;
RESULT 961
ID AEF71404 standard; protein; 717 AA.
DE Human immunoglobulin superfamily, member 9, protein SEQ ID NO:55.
PN WO2006014999-A2.
PD 09-FEB-2006.
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
Query Match 12.5%; Score 226; DB 10; Length 717;
Best Local Similarity 24.8%; Pred. No. 2.8e-10;
RESULT 962
ID ADN22360 standard; protein; 6642 AA.
DE Bacterial polypeptide #5013.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOX/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 12.5%; Score 226; DB 8; Length 6642;
Best Local Similarity 23.7%; Pred. No. 5.8e-09;
RESULT 963
ID AAR92718 standard; protein; 478 AA.
DE Mouse muscle-localized protein-tyrosine-kinase receptor 5' fragment.
PN WO9602644-A1.
PD 01-FEB-1996.
PA (GEMY) GENETICS INST INC.
Query Match 12.5%; Score 225.5; DB 2; Length 478;
Best Local Similarity 24.8%; Pred. No. 1.7e-10;
RESULT 964
ID AAR92716 standard; protein; 860 AA.
DE Mouse muscle-localised protein-tyrosine-kinase receptor-1 isoform.
PN WO9602644-A1.
PD 01-FEB-1996.
PA (GEMY) GENETICS INST INC.
Query Match 12.5%; Score 225.5; DB 2; Length 860;
Best Local Similarity 24.8%; Pred. No. 3.9e-10;
RESULT 965
ID AAR92717 standard; protein; 868 AA.
DE Mouse muscle-localised protein-tyrosine-kinase receptor-2 isoform.
PN WO9602644-A1.
PD 01-FEB-1996.
PA (GEMY) GENETICS INST INC.
Query Match 12.5%; Score 225.5; DB 2; Length 868;
Best Local Similarity 24.8%; Pred. No. 4e-10;
RESULT 966
ID ABJ10922 standard; protein; 869 AA.
DE Human secreted protein (SECP) #18.
PN WO200270669-A2.
PD 12-SEP-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 12.5%; Score 225.5; DB 5; Length 869;
Best Local Similarity 29.5%; Pred. No. 4e-10;
RESULT 967
ID AAE34390 standard; protein; 4391 AA.
DE Human perlecan protein.

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PN WO200295415-A2.
PD 28-NOV-2002.
PA (OSTE-) OSTEOMETER BIO TECH AS.
  Query Match      12.5%; Score 225; DB 6; Length 4391;
  Best Local Similarity 25.7%; Pred. No. 4e-09;
  RESULT 968
ID ADM16038 standard; protein; 477 AA.
DE Human FGFR5 splice variant #4, SEQ ID 23.
PN US2005009750-A1.
PD 13-JAN-2005.
PA (GENE-) GENESIS RES & DEV CORP LTD.
  Query Match      12.4%; Score 224.5; DB 9; Length 477;
  Best Local Similarity 22.7%; Pred. No. 2.1e-10;
  RESULT 969
ID AEA05858 standard; protein; 477 AA.
DE Human fibroblast growth factor receptor 5 splice variant, SEQ:23.
PN US2005112642-A1.
PD 26-MAY-2005.
PA (GENE-) GENESIS RES & DEV CORP LTD.
  Query Match      12.4%; Score 224.5; DB 9; Length 477;
  Best Local Similarity 22.7%; Pred. No. 2.1e-10;
  RESULT 970
ID ABG74129 standard; protein; 537 AA.
DE Human hMusk-R deletion mutant mMusk-RI.
PN US2002150876-A1.
PD 17-OCT-2002.
PA (PIPP/) PIPPIG S D.
PA (VERE/) VERES G.
  Query Match      12.4%; Score 224.5; DB 4; Length 537;
  Best Local Similarity 26.0%; Pred. No. 2.5e-10;
  RESULT 971
ID AAG77857 standard; protein; 537 AA.
DE Mutant protein mMusk-RI.
PN WO200172834-A1.
PD 04-OCT-2001.
PA (NOVS ) NOVARTIS AG.
PA (NOVS ) NOVARTIS-ERFINDUNGEN VERW GES MBH.
  Query Match      12.4%; Score 224.5; DB 4; Length 537;
  Best Local Similarity 26.0%; Pred. No. 2.5e-10;
  RESULT 972
ID ABG74130 standard; protein; 576 AA.
DE Human hMusk-R deletion mutant mMusk-RII.
PN US2002150876-A1.
PD 17-OCT-2002.
PA (PIPP/) PIPPIG S D.
PA (VERE/) VERES G.
  Query Match      12.4%; Score 224.5; DB 4; Length 576;
  Best Local Similarity 26.0%; Pred. No. 2.8e-10;
  RESULT 973
ID AAG77858 standard; protein; 576 AA.
DE Mutant protein mMusk-RII.
PN WO200172834-A1.
PD 04-OCT-2001.
PA (NOVS ) NOVARTIS AG.
PA (NOVS ) NOVARTIS-ERFINDUNGEN VERW GES MBH.
  Query Match      12.4%; Score 224.5; DB 4; Length 576;
  Best Local Similarity 26.0%; Pred. No. 2.8e-10;
  RESULT 974
ID ABG74128 standard; protein; 869 AA.
DE Human muscle specific tyrosine kinase receptor, hMusk-R.
PN US2002150876-A1.
PD 17-OCT-2002.
PA (PIPP/) PIPPIG S D.
PA (VERE/) VERES G.
  Query Match      12.4%; Score 224.5; DB 4; Length 869;
  Best Local Similarity 26.0%; Pred. No. 4.8e-10;
  RESULT 975
ID AAB68421 standard; protein; 869 AA.
DE Amino acid sequence of a human Musk-R polypeptide.
PN WO200136659-A2.
PD 25-MAY-2001.
PA (NOVS ) NOVARTIS AG.
PA (NOVS ) NOVARTIS-ERFINDUNGEN VERW GES MBH.
  Query Match      12.4%; Score 224.5; DB 4; Length 869;
  Best Local Similarity 26.0%; Pred. No. 4.8e-10;
  RESULT 976
ID AAG77856 standard; protein; 869 AA.
DE Protein of muscle specific tyrosine kinase receptor (hMusk-R).
PN WO200172834-A1.
PD 04-OCT-2001.
PA (NOVS ) NOVARTIS AG.
PA (NOVS ) NOVARTIS-ERFINDUNGEN VERW GES MBH.
  Query Match      12.4%; Score 224.5; DB 4; Length 869;
  Best Local Similarity 26.0%; Pred. No. 4.8e-10;
  RESULT 977
ID ADS17276 standard; protein; 869 AA.
DE Human muscle specific tyrosine kinase receptor (Musk-R) protein fragment.
PN US6790614-B1.
PD 14-SEP-2004.
PA (NOVS ) NOVARTIS AG.
  Query Match      12.4%; Score 224.5; DB 8; Length 869;
  Best Local Similarity 26.0%; Pred. No. 4.8e-10;
  RESULT 978
ID ABG22633 standard; protein; 981 AA.
DE Novel human diagnostic protein #22624.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
  Query Match      12.4%; Score 224.5; DB 4; Length 981;
  Best Local Similarity 23.9%; Pred. No. 5.7e-10;
  RESULT 979
ID ADR08740 standard; protein; 1113 AA.
DE Human protein useful for treating neurological disease Seq 2246.
PN EPI47413-A2.
PD 18-AUG-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
  Query Match      12.4%; Score 224.5; DB 8; Length 1113;
  Best Local Similarity 25.3%; Pred. No. 6.8e-10;
  RESULT 980
ID ADL16578 standard; protein; 1171 AA.
DE Human 282PIG3 polypeptide #31.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
  Query Match      12.4%; Score 224.5; DB 8; Length 1171;
  Best Local Similarity 25.3%; Pred. No. 7.3e-10;
  RESULT 981
ID ADL16624 standard; protein; 1171 AA.
DE Human 282PIG3 polypeptide #56.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
  Query Match      12.4%; Score 224.5; DB 8; Length 1171;
  Best Local Similarity 25.3%; Pred. No. 7.3e-10;
  RESULT 982
ID ADL16580 standard; protein; 1171 AA.
DE Human 282PIG3 polypeptide #33.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
  Query Match      12.4%; Score 224.5; DB 8; Length 1171;
  Best Local Similarity 25.3%; Pred. No. 7.3e-10;
  RESULT 983
ID ADL16429 standard; protein; 1171 AA.
DE Human 282PIG3 polypeptide #2.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
  Query Match      12.4%; Score 224.5; DB 8; Length 1171;
  Best Local Similarity 25.3%; Pred. No. 7.3e-10;
  RESULT 984
ID ADL16445 standard; protein; 1171 AA.
DE Human 282PIG3 polypeptide #11.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.

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Query Match
Best Local Similarity 12.4%; Score 224.5; DB 8; Length 1171;
RESULT 985
ID ADE55236 standard; protein; 1224 AA.
DE Human protein AAB60937, SEQ ID NO 1049.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO ) GEN HOSPITAL CORP.
PA (FARB ) BAYER AG.
Query Match
Best Local Similarity 12.4%; Score 224.5; DB 7; Length 1224;
RESULT 986
ID ADL15032 standard; protein; 1224 AA.
DE Human neural cell adhesion molecule protein for cancer treatment.
PN WO2003068268-A2.
PD 21-AUG-2003.
PA (BIOI-) BIOINVENT INT AB.
Query Match
Best Local Similarity 12.4%; Score 224.5; DB 7; Length 1224;
RESULT 987
ID ADU75519 standard; protein; 1224 AA.
DE Marker gene related amino acid sequence SEQ ID NO:771.
PN EPI394274-A2.
PD 03-MAR-2004.
PA (GENO-) GENOX RES INC.
Query Match
Best Local Similarity 12.4%; Score 224.5; DB 8; Length 1224;
RESULT 988
ID ADL16454 standard; protein; 1224 AA.
DE Human 282P1G3 polypeptide #20.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Query Match
Best Local Similarity 12.4%; Score 224.5; DB 8; Length 1224;
RESULT 989
ID ADN04062 standard; protein; 1224 AA.
DE Antipneumatic protein sequence #226.
PN WO2004028479-A2.
PD 08-APR-2004.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 12.4%; Score 224.5; DB 8; Length 1224;
RESULT 990
ID ADQ19766 standard; protein; 1224 AA.
DE Human soft tissue sarcoma-upregulated protein - SEQ ID 2585.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match
Best Local Similarity 12.4%; Score 224.5; DB 8; Length 1224;
RESULT 991
ID ADRI14776 standard; protein; 1224 AA.
DE Amino acid sequence of human MAPCA orthologue #8.
PN WO2004066948-A2.
PD 12-AUG-2004.
PA (EXEL-) EXELIXIS INC.
Query Match
Best Local Similarity 12.4%; Score 224.5; DB 8; Length 1224;
RESULT 992
ID ADP29420 standard; protein; 1583 AA.
DE Human secreted protein SEQ ID #1418.
PN WO2004035732-A2.
PD 29-APR-2004.
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
Query Match
Best Local Similarity 12.4%; Score 224.5; DB 8; Length 1583;
RESULT 993
ID ADP29354 standard; protein; 1583 AA.
DE Human secreted protein SEQ ID #1352.
PN WO2004035732-A2.
PD 29-APR-2004.
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
Query Match
Best Local Similarity 12.4%; Score 224.5; DB 8; Length 1583;
RESULT 994
ID ABG20008 standard; protein; 1645 AA.
DE Novel human diagnostic protein #19999.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 12.4%; Score 224.5; DB 4; Length 1645;
RESULT 995
ID ABG22631 standard; protein; 1765 AA.
DE Novel human diagnostic protein #22622.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 12.4%; Score 224.5; DB 4; Length 1765;
RESULT 996
ID ABG12017 standard; protein; 1944 AA.
DE Novel human diagnostic protein #12008.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 12.4%; Score 224.5; DB 4; Length 1944;
RESULT 997
ID AAE30259 standard; peptide; 68 AA.
DE Human LP289 protein immunoglobulin-like domain #1.
PN WO200274906-A2.
PD 26-SEP-2002.
PA (ELIL ) LILLY & CO ELI.
Query Match
Best Local Similarity 12.4%; Score 224; DB 6; Length 68;
RESULT 998
ID ABG02117 standard; protein; 434 AA.
DE Novel human diagnostic protein #2108.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 12.4%; Score 224; DB 4; Length 434;
RESULT 999
ID RAM93829 standard; protein; 697 AA.
DE Human polypeptide, SEQ ID NO: 3893.
PN EPI130094-A2.
PD 05-SEP-2001.
PA (HELI-) HELIX RES INST.
Query Match
Best Local Similarity 12.4%; Score 224; DB 4; Length 697;
RESULT 1000
ID ADL31860 standard; protein; 697 AA.
DE Human protein encoded by a full length cDNA clone SeqID 3893.
PN EPI396543-A2.
PD 10-MAR-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match
Best Local Similarity 12.4%; Score 224; DB 8; Length 697;
RESULT 1001
ID ABG02019 standard; protein; 737 AA.
DE Novel human diagnostic protein #2010.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 12.4%; Score 224; DB 4; Length 737;
RESULT 1002
ID AAY08095 standard; protein; 1059 AA.
DE Human PRO335 protein.
PN WO9914241-A2.
PD 25-MAR-1999.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 12.4%; Score 224; DB 2; Length 1059;
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Best Local Similarity 23.9%; Pred. No. 7e-10;
RESULT 1003
ID AAY13393 standard; protein; 1059 AA.
DE Amino acid sequence of protein PRO335.
PN WO9914328-A2.
PD 25-MAR-1999.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 2; Length 1059;
Best Local Similarity 23.9%; Pred. No. 7e-10;
RESULT 1004
ID AAY70672 standard; protein; 1059 AA.
DE Human PRO335 protein.
PN WO200015797-A2.
PD 23-MAR-2000.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 3; Length 1059;
Best Local Similarity 23.9%; Pred. No. 7e-10;
RESULT 1005
ID ADC78602 standard; protein; 1059 AA.
DE Human PRO335 protein.
PN WO200015796-A2.
PD 23-MAR-2000.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 3; Length 1059;
Best Local Similarity 23.9%; Pred. No. 7e-10;
RESULT 1006
ID AAB80261 standard; protein; 1059 AA.
DE Human PRO335 protein.
PN WO200104311-A1.
PD 18-JAN-2001.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 4; Length 1059;
Best Local Similarity 23.9%; Pred. No. 7e-10;
RESULT 1007
ID AAU00825 standard; protein; 1059 AA.
DE Human immune response protein PRO335 (UNQ287).
PN WO200119991-A1.
PD 22-MAR-2001.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 4; Length 1059;
Best Local Similarity 23.9%; Pred. No. 7e-10;
RESULT 1008
ID ABU71639 standard; protein; 1059 AA.
DE Human PRO polypeptide #50.
PN US2002146709-A1.
PD 10-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1059;
Best Local Similarity 23.9%; Pred. No. 7e-10;
RESULT 1009
ID ABU71494 standard; protein; 1059 AA.
DE Human PRO polypeptide #50.
PN US2002192659-A1.
PD 19-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1059;
Best Local Similarity 23.9%; Pred. No. 7e-10;
RESULT 1010
ID ABU71940 standard; protein; 1059 AA.
DE Human secreted/transmembrane protein PRO335.
PN US2003003530-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1059;
Best Local Similarity 23.9%; Pred. No. 7e-10;
RESULT 1011
ID ABO01823 standard; protein; 1059 AA.
DE Novel human secreted and transmembrane protein PRO335.
PN US2002197671-A1.
PD 26-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1059;
Best Local Similarity 23.9%; Pred. No. 7e-10;
RESULT 1012
ID ABU54396 standard; protein; 1059 AA.
DE Human secreted/transmembrane protein PRO335.
PN US2002132240-A1.
PD 19-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1059;
Best Local Similarity 23.9%; Pred. No. 7e-10;
RESULT 1013
ID AB047411 standard; protein; 1059 AA.
DE Human secreted/transmembrane polypeptide PRO335.
PN US2003044839-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1059;
Best Local Similarity 23.9%; Pred. No. 7e-10;
RESULT 1014
ID ABU64548 standard; protein; 1059 AA.
DE Human secreted/transmembrane protein, #52.
PN US2002160374-A1.
PD 31-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1059;
Best Local Similarity 23.9%; Pred. No. 7e-10;
RESULT 1015
ID ABU67394 standard; protein; 1059 AA.
DE Human secreted protein PRO335.
PN US2003023054-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1059;
Best Local Similarity 23.9%; Pred. No. 7e-10;
RESULT 1016
ID AB014914 standard; protein; 1059 AA.
DE Human secreted / transmembrane polypeptide PRO335.
PN US2003030600-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1059;
Best Local Similarity 23.9%; Pred. No. 7e-10;
RESULT 1017
ID ABU69671 standard; protein; 1059 AA.
DE Novel human secreted and transmembrane protein PRO335.
PN US2003017463-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1059;
Best Local Similarity 23.9%; Pred. No. 7e-10;
RESULT 1018
ID AB014853 standard; protein; 1059 AA.
DE Human secreted / transmembrane polypeptide PRO335.
PN US2003027143-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1059;
Best Local Similarity 23.9%; Pred. No. 7e-10;
RESULT 1019
ID ADB29495 standard; protein; 1059 AA.
DE Human secreted/transmembrane protein, #54.
PN US2003092002-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1059;
Best Local Similarity 23.9%; Pred. No. 7e-10;
RESULT 1020
ID ADA18351 standard; protein; 1059 AA.
DE Human secreted/transmembrane protein, #54.
PN US2003039971-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1059;
Best Local Similarity 23.9%; Pred. No. 7e-10;
RESULT 1021

ID ABO32805 standard; protein; 1059 AA.
DE Human secreted/transmembrane protein PRO335.
PN US2003045693-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1059;
Best Local Similarity 23.9%; Pred. No. 7e-10;
RESULT 1022
ID ABO34865 standard; protein; 1059 AA.
DE Human PRO polypeptide #50.
PN US2003044793-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1059;
Best Local Similarity 23.9%; Pred. No. 7e-10;
RESULT 1023
ID ADA16326 standard; protein; 1059 AA.
DE Human secreted/transmembrane protein, #54.
PN US2003049621-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1059;
Best Local Similarity 23.9%; Pred. No. 7e-10;
RESULT 1024
ID ADA42471 standard; protein; 1059 AA.
DE Human secreted/transmembrane protein, #54.
PN US2003054401-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1059;
Best Local Similarity 23.9%; Pred. No. 7e-10;
RESULT 1025
ID ABO17543 standard; protein; 1059 AA.
DE Human PRO polypeptide #50.
PN US2003064367-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1059;
Best Local Similarity 23.9%; Pred. No. 7e-10;
RESULT 1026
ID ADA16750 standard; protein; 1059 AA.
DE Human secreted/transmembrane protein, #54.
PN US2003039969-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1059;
Best Local Similarity 23.9%; Pred. No. 7e-10;
RESULT 1027
ID ADA13179 standard; protein; 1059 AA.
DE Human secreted/transmembrane protein, #54.
PN US2003049622-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1059;
Best Local Similarity 23.9%; Pred. No. 7e-10;
RESULT 1028
ID ADA42047 standard; protein; 1059 AA.
DE Human secreted/transmembrane protein, #54.
PN US2003082540-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1059;
Best Local Similarity 23.9%; Pred. No. 7e-10;
RESULT 1029
ID ADA17394 standard; protein; 1059 AA.
DE Human secreted/transmembrane protein, #54.
PN US2003017498-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1059;
Best Local Similarity 23.9%; Pred. No. 7e-10;
RESULT 1030
ID ADA42897 standard; protein; 1059 AA.
DE Human secreted/transmembrane protein, #54.
PN US2003054351-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1059;
Best Local Similarity 23.9%; Pred. No. 7e-10;
RESULT 1031
ID ABO17604 standard; protein; 1059 AA.
DE Human PRO polypeptide #50.
PN US2003064923-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1059;
Best Local Similarity 23.9%; Pred. No. 7e-10;
RESULT 1032
ID ADB77816 standard; protein; 1059 AA.
DE Human secreted/transmembrane protein, #54.
PN US2003077654-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1059;
Best Local Similarity 23.9%; Pred. No. 7e-10;
RESULT 1033
ID ADB74952 standard; protein; 1059 AA.
DE Human secreted/transmembrane protein, #54.
PN US2003082542-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1059;
Best Local Similarity 23.9%; Pred. No. 7e-10;
RESULT 1034
ID ADC28598 standard; protein; 1059 AA.
DE Human secreted/transmembrane protein, #54.
PN US2003059772-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1059;
Best Local Similarity 23.9%; Pred. No. 7e-10;
RESULT 1035
ID ADC39798 standard; protein; 1059 AA.
DE Human secreted/transmembrane protein, #54.
PN US2003059828-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1059;
Best Local Similarity 23.9%; Pred. No. 7e-10;
RESULT 1036
ID ADC40312 standard; protein; 1059 AA.
DE Human secreted/transmembrane protein, #54.
PN US2003059829-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1059;
Best Local Similarity 23.9%; Pred. No. 7e-10;
RESULT 1037
ID ADC13136 standard; protein; 1059 AA.
DE Human secreted/transmembrane protein, #54.
PN US2003036061-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1059;
Best Local Similarity 23.9%; Pred. No. 7e-10;
RESULT 1038
ID ADC34436 standard; protein; 1059 AA.
DE Human secreted/transmembrane protein, #54.
PN US2003036094-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1059;
Best Local Similarity 23.9%; Pred. No. 7e-10;
RESULT 1039
ID ADC29491 standard; protein; 1059 AA.
DE Human secreted/transmembrane protein, #54.

PD US2003049676-A1.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1059;
Best Local Similarity 23.9%; Pred. No. 7e-10;
RESULT 1040
ID ADC29022 standard; protein; 1059 AA.
DE Human secreted/transmembrane protein, #54.
PN US2003049677-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1059;
Best Local Similarity 23.9%; Pred. No. 7e-10;
RESULT 1041
ID ADC40907 standard; protein; 1059 AA.
DE Human secreted/transmembrane protein, #54.
PN US2003054400-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1059;
Best Local Similarity 23.9%; Pred. No. 7e-10;
RESULT 1042
ID ADC19564 standard; protein; 1059 AA.
DE Human secreted/transmembrane protein, #54.
PN US2003054441-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1059;
Best Local Similarity 23.9%; Pred. No. 7e-10;
RESULT 1043
ID ADC34012 standard; protein; 1059 AA.
DE Human secreted/transmembrane protein, #54.
PN US2003073077-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1059;
Best Local Similarity 23.9%; Pred. No. 7e-10;
RESULT 1044
ID ADC13082 standard; protein; 1059 AA.
DE Human secreted/transmembrane protein, #54.
PN US2003073079-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1059;
Best Local Similarity 23.9%; Pred. No. 7e-10;
RESULT 1045
ID ADC12534 standard; protein; 1059 AA.
DE Human secreted/transmembrane protein, #54.
PN US2003082541-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1059;
Best Local Similarity 23.9%; Pred. No. 7e-10;
RESULT 1046
ID ADD05089 standard; protein; 1059 AA.
DE Human secreted/transmembrane protein, #54.
PN US2003104469-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1059;
Best Local Similarity 23.9%; Pred. No. 7e-10;
RESULT 1047
ID ADD04095 standard; protein; 1059 AA.
DE Human secreted/transmembrane protein, #54.
PN US2003104381-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1059;
Best Local Similarity 23.9%; Pred. No. 7e-10;
RESULT 1048
ID ADD03671 standard; protein; 1059 AA.
DE Human secreted/transmembrane protein, #54.
PN US2003108983-A1.

PD 12-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1059;
Best Local Similarity 23.9%; Pred. No. 7e-10;
RESULT 1049
ID ADE34923 standard; protein; 1059 AA.
DE Human secreted/transmembrane protein, #54.
PN US2003077583-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1059;
Best Local Similarity 23.9%; Pred. No. 7e-10;
RESULT 1050
ID ADH59406 standard; protein; 1059 AA.
DE Human secreted/transmembrane protein, #54.
PN US2003039972-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1059;
Best Local Similarity 23.9%; Pred. No. 7e-10;
RESULT 1051
ID ADI38185 standard; protein; 1059 AA.
DE Human secreted/transmembrane protein, #54.
PN US2003054352-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1059;
Best Local Similarity 23.9%; Pred. No. 7e-10;
RESULT 1052
ID ADJ26453 standard; protein; 1059 AA.
DE Human secreted/transmembrane protein, #54.
PN US2003054349-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1059;
Best Local Similarity 23.9%; Pred. No. 7e-10;
RESULT 1053
ID ADE79368 standard; protein; 1059 AA.
DE Human secreted/transmembrane protein, #54.
PN US2003135025-A1.
PD 17-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1059;
Best Local Similarity 23.9%; Pred. No. 7e-10;
RESULT 1054
ID ADE79792 standard; protein; 1059 AA.
DE Human secreted/transmembrane protein, #54.
PN US2003130489-A1.
PD 10-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1059;
Best Local Similarity 23.9%; Pred. No. 7e-10;
RESULT 1055
ID ADE73468 standard; protein; 1059 AA.
DE Human secreted/transmembrane protein, #54.
PN US2003129592-A1.
PD 10-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1059;
Best Local Similarity 23.9%; Pred. No. 7e-10;
RESULT 1056
ID ADE74003 standard; protein; 1059 AA.
DE Human secreted/transmembrane protein, #54.
PN US2003148370-A1.
PD 07-AUG-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1059;
Best Local Similarity 23.9%; Pred. No. 7e-10;
RESULT 1057
ID ADE99557 standard; protein; 1059 AA.
DE Human secreted/transmembrane protein, #54.
PN US2003211576-A1.
PD 13-NOV-2003.

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PA (GETH) GENENTECH INC.
 Query Match 12.4%; Score 224; DB 8; Length 1059;
 Best Local Similarity 23.9%; Pred. No. 7e-10;
 RESULT 1074
 ID ADH60662 standard; protein; 1059 AA.
 DE Human secreted/transmembrane protein, #54.
 PN US2004023331-A1.
 PD 05-FEB-2004.
 PA (DESN/) DESNOYERS L.
 PA (GODD/) GODDARD A.
 PA (GODO/) GODOWSKI P J.
 PA (GURN/) GURNEY A L.
 PA (MATH/) MATHER J P.
 PA (WILL/) WILLIAMS P M.
 PA (WOOD/) WOOD W I.
 Query Match 12.4%; Score 224; DB 8; Length 1059;
 Best Local Similarity 23.9%; Pred. No. 7e-10;
 RESULT 1075
 ID ADJ99719 standard; protein; 1059 AA.
 DE Human secreted/transmembrane protein, #54.
 PN US2003187238-A1.
 PD 02-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 12.4%; Score 224; DB 8; Length 1059;
 Best Local Similarity 23.9%; Pred. No. 7e-10;
 RESULT 1076
 ID ADL08912 standard; protein; 1059 AA.
 DE Human secreted/transmembrane protein, #54.
 PN US2003186358-A1.
 PD 02-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 12.4%; Score 224; DB 8; Length 1059;
 Best Local Similarity 23.9%; Pred. No. 7e-10;
 RESULT 1077
 ID ADM25253 standard; protein; 1059 AA.
 DE Human secreted/transmembrane protein, #54.
 PN US2003096233-A1.
 PD 22-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 12.4%; Score 224; DB 8; Length 1059;
 Best Local Similarity 23.9%; Pred. No. 7e-10;
 RESULT 1078
 ID ADM30003 standard; protein; 1059 AA.
 DE Human secreted/transmembrane protein, #54.
 PN US2003190611-A1.
 PD 09-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 12.4%; Score 224; DB 8; Length 1059;
 Best Local Similarity 23.9%; Pred. No. 7e-10;
 RESULT 1079
 ID ADO06325 standard; protein; 1059 AA.
 DE Human PRO polypeptide #50.
 PN US6686451-B1.
 PD 03-FEB-2004.
 PA (GETH) GENENTECH INC.
 Query Match 12.4%; Score 224; DB 8; Length 1059;
 Best Local Similarity 23.9%; Pred. No. 7e-10;
 RESULT 1080
 ID ADRI1177 standard; protein; 1059 AA.
 DE Human secreted/transmembrane protein, #54.
 PN US2004137561-A1.
 PD 15-JUL-2004.
 PA (GETH) GENENTECH INC.
 Query Match 12.4%; Score 224; DB 8; Length 1059;
 Best Local Similarity 23.9%; Pred. No. 7e-10;
 RESULT 1081
 ID ADRI8086 standard; protein; 1059 AA.
 DE Human secreted/transmembrane protein, #54.
 PN US2004147017-A1.
 PD 29-JUL-2004.
 PA (ASHK/) ASHKENAZI A.
 PA (BOTS/) BOTSTEIN D.
 PA (DESN/) DESNOYERS L.

PA (EATO/) EATON D L.
 PA (FERR/) FERRARA N.
 PA (FILV/) FILVAROFF E.
 PA (FONG/) FONG S.
 PA (GAOW/) GAO W.
 PA (GERB/) GERBER H.
 PA (GERR/) GERRITSEN M E.
 PA (GODD/) GODDARD A.
 PA (GODO/) GODOWSKI P J.
 PA (GRIM/) GRIMALDI C J.
 PA (GURN/) GURNEY A L.
 PA (HILL/) HILLAN K J.
 PA (KLJA/) KLJAVIN I J.
 PA (MATH/) MATHER J P.
 PA (PANJ/) PAN J.
 PA (PAON/) PAONI N F.
 PA (ROYM/) ROY M A.
 PA (STEW/) STEWART T A.
 PA (TUMA/) TUMAS D.
 PA (WILL/) WILLIAMS P M.
 PA (WOOD/) WOOD W I.
 Query Match 12.4%; Score 224; DB 8; Length 1059;
 Best Local Similarity 23.9%; Pred. No. 7e-10;
 RESULT 1082
 ID ADS74725 standard; protein; 1059 AA.
 DE Human secreted/transmembrane protein #54.
 PN US2004185531-A1.
 PD 23-SEP-2004.
 PA (ASHK/) ASHKENAZI A.
 PA (BOTS/) BOTSTEIN D.
 PA (DESN/) DESNOYERS L.
 PA (EATO/) EATON D L.
 PA (FERR/) FERRARA N.
 PA (FILV/) FILVAROFF E.
 PA (FONG/) FONG S.
 PA (GERB/) GAO W.
 PA (GERR/) GERRITSEN M E.
 PA (GODD/) GODDARD A.
 PA (GODO/) GODOWSKI P J.
 PA (GRIM/) GRIMALDI C J.
 PA (GURN/) GURNEY A L.
 PA (HILL/) HILLAN K J.
 PA (KLJA/) KLJAVIN I J.
 PA (MATH/) MATHER J P.
 PA (PANJ/) PAN J.
 PA (PAON/) PAONI N F.
 PA (ROYM/) ROY M A.
 PA (STEW/) STEWART T A.
 PA (TUMA/) TUMAS D.
 PA (WILL/) WILLIAMS P M.
 PA (WOOD/) WOOD W I.
 Query Match 12.4%; Score 224; DB 8; Length 1059;
 Best Local Similarity 23.9%; Pred. No. 7e-10;
 RESULT 1083
 ID ADT03762 standard; protein; 1059 AA.
 DE Human secreted/transmembrane protein, #54.
 PN US2003152922-A1.
 PD 14-AUG-2003.
 PA (GETH) GENENTECH INC.
 Query Match 12.4%; Score 224; DB 8; Length 1059;
 Best Local Similarity 23.9%; Pred. No. 7e-10;
 RESULT 1084
 ID AEA38000 standard; protein; 1059 AA.
 DE Human secreted/transmembrane protein, #54.
 PN US2005112725-A1.
 PD 26-MAY-2005.
 PA (GETH) GENENTECH INC.
 Query Match 12.4%; Score 224; DB 9; Length 1059;
 Best Local Similarity 23.9%; Pred. No. 7e-10;
 RESULT 1085
 ID AED24034 standard; protein; 1059 AA.
 DE Human secreted protein PRO 335, SEQ ID 290.

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PN US2005214904-A1.
PD 29-SEP-2005.
PA (GETH ) GENENTECH INC.
  Query Match 12.4%; Score 224; DB 9; Length 1059;
  Best Local Similarity 23.9%; Pred. No. 7e-10;
RESULT 1086
ID ABE69203 standard; protein; 1059 AA.
DE Leucine rich repeat protein homologous PRO335 protein, SEQ ID 290.
PN US6974689-B1.
PD 13-DEC-2005.
PA (GETH ) GENENTECH INC.
  Query Match 12.4%; Score 224; DB 10; Length 1059;
  Best Local Similarity 23.9%; Pred. No. 7e-10;
RESULT 1087
ID AAY08114 standard; protein; 1119 AA.
DE Human PRO326 protein.
PN WO9914241-A2.
PD 25-MAR-1999.
PA (GETH ) GENENTECH INC.
  Query Match 12.4%; Score 224; DB 2; Length 1119;
  Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1088
ID AAY70674 standard; protein; 1119 AA.
DE Human PRO326 protein.
PN WO200015797-A2.
PD 23-MAR-2000.
PA (GETH ) GENENTECH INC.
  Query Match 12.4%; Score 224; DB 3; Length 1119;
  Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1089
ID ADC78606 standard; protein; 1119 AA.
DE Human PRO326 protein.
PN WO200015796-A2.
PD 23-MAR-2000.
PA (GETH ) GENENTECH INC.
  Query Match 12.4%; Score 224; DB 3; Length 1119;
  Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1090
ID AAB80263 standard; protein; 1119 AA.
DE Human PRO326 protein.
PN WO200104311-A1.
PD 18-JAN-2001.
PA (GETH ) GENENTECH INC.
  Query Match 12.4%; Score 224; DB 4; Length 1119;
  Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1091
ID AAB48162 standard; protein; 1119 AA.
DE Human PRO326 polypeptide.
PN WO200075316-A1.
PD 14-DEC-2000.
PA (GETH ) GENENTECH INC.
  Query Match 12.4%; Score 224; DB 4; Length 1119;
  Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1092
ID AAU00827 standard; protein; 1119 AA.
DE Human immune response protein PRO326 (UNQ287).
PN WO200119991-A1.
PD 22-MAR-2001.
PA (GETH ) GENENTECH INC.
  Query Match 12.4%; Score 224; DB 4; Length 1119;
  Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1093
ID AAU12347 standard; protein; 1119 AA.
DE Human PRO326 polypeptide sequence.
PN WO200140466-A2.
PD 07-JUN-2001.
PA (GETH ) GENENTECH INC.
  Query Match 12.4%; Score 224; DB 4; Length 1119;
  Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1094
ID ABU71641 standard; protein; 1119 AA.
DE Human PRO polypeptide #52.
PN US2002146709-A1.
PD 23-SEP-2005.
PA (GETH ) GENENTECH INC.
  Query Match 12.4%; Score 224; DB 6; Length 1119;
  Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1095
ID ABO17791 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003032156-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
  Query Match 12.4%; Score 224; DB 6; Length 1119;
  Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1096
ID ABU71496 standard; protein; 1119 AA.
DE Human PRO polypeptide #52.
PN US2002192659-A1.
PD 19-DEC-2002.
PA (GETH ) GENENTECH INC.
  Query Match 12.4%; Score 224; DB 6; Length 1119;
  Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1097
ID ABU81045 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003004311-A1.
PD 02-JAN-2003.
PA (GETH ) GENENTECH INC.
  Query Match 12.4%; Score 224; DB 6; Length 1119;
  Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1098
ID ABU71942 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein PRO326.
PN US2003003530-A1.
PD 02-JAN-2003.
PA (GETH ) GENENTECH INC.
  Query Match 12.4%; Score 224; DB 6; Length 1119;
  Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1099
ID ABO01825 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2002197671-A1.
PD 26-DEC-2002.
PA (GETH ) GENENTECH INC.
  Query Match 12.4%; Score 224; DB 6; Length 1119;
  Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1100
ID ABU66745 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003036180-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
  Query Match 12.4%; Score 224; DB 6; Length 1119;
  Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1101
ID ABU54398 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein PRO326.
PN US2002132240-A1.
PD 19-SEP-2002.
PA (GETH ) GENENTECH INC.
  Query Match 12.4%; Score 224; DB 6; Length 1119;
  Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1102
ID ABO47413 standard; protein; 1119 AA.
DE Human secreted/transmembrane polypeptide PRO326.
PN US2003044839-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
  Query Match 12.4%; Score 224; DB 6; Length 1119;
  Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1103
ID ABUS9826 standard; protein; 1119 AA.
DE Novel secreted and transmembrane protein PRO326.
PN US2003017563-A1.
PD 23-JAN-2003.
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PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1104
ID ABO25016 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein (PRO) #176.
PN US2003036179-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1105
ID ABU64550 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein, #54.
PN US2002160374-A1.
PD 31-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1106
ID ABU67396 standard; protein; 1119 AA.
DE Human secreted protein PRO326.
PN US2003023054-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1107
ID ABO14916 standard; protein; 1119 AA.
DE Human secreted / transmembrane polypeptide PRO326.
PN US2003036060-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1108
ID ABU67021 standard; protein; 1119 AA.
DE Human secreted/transmembrane, PRO, protein SEQ ID 352.
PN US2003032155-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1109
ID ABU69673 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003017463-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1110
ID ABO14855 standard; protein; 1119 AA.
DE Human secreted / transmembrane polypeptide PRO326.
PN US2003027143-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1111
ID ADA45871 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003023238-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1112
ID ADA76302 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003073212-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.

Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1113
ID ADE29499 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein, #56.
PN US2003092002-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1114
ID ADA18952 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003054517-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1115
ID ADA61575 standard; protein; 1119 AA.
DE Homo sapiens.
PN US2003049816-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1116
ID ADB19360 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003068796-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1117
ID ADB27901 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003082704-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1118
ID ADA86380 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003082711-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1119
ID ADB15944 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003087350-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1120
ID ADA47730 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003073215-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1121
ID ADA18355 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein, #56.
PN US2003039971-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;

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Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1122
ID ABO32807 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein PRO326.
PN US2003045693-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1123
ID ABO32808 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein PRO332.
PN US2003045693-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1124
ID ADA67525 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003068795-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1125
ID ADB30532 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003068794-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1126
ID ADA85828 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003082693-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1127
ID ADA97040 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003082705-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1128
ID ADA79344 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003082763-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1129
ID ADA87483 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003087345-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1130
ID ADB16685 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003087349-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1131
ID ABO34867 standard; protein; 1119 AA.
DE Human PRO polypeptide #52.
PN US2003044793-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1132
ID ADA16330 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein, #56.
PN US2003049621-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1133
ID ADA91777 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003082694-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1134
ID ADB14840 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003087351-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1135
ID ADB18801 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003073211-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1136
ID ADA94016 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US200307722-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1137
ID ADB19912 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003082691-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1138
ID ADB13224 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003082710-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1139
ID ABO43324 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003044945-A1.
PD 08-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1140
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ID ADA74478 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003068798-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1141
ID ADA42475 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein, #56.
PN US2003054401-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1142
ID ADB24711 standard; protein; 1119 AA.
DE Human PRO polypeptide SEQ ID NO 352.
PN US2003077713-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1143
ID ADA82235 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003082701-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1144
ID ADA75198 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003073216-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1145
ID ADA85276 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003082695-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1146
ID ADA84724 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003082708-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1147
ID ABO17545 standard; protein; 1119 AA.
DE Human PRO polypeptide #52.
PN US2003064367-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1148
ID ADB29980 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003073214-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1149
ID ADA80508 standard; protein; 1119 AA.

DE Human PRO polypeptide #176.
PN US2003082761-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1150
ID ADA75750 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003082703-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1151
ID ADA46975 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003073210-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1152
ID ADB25271 standard; protein; 1119 AA.
DE Human PRO polypeptide SEQ ID NO 352.
PN US2003077715-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1153
ID ADA93447 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003077721-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1154
ID ADB26797 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003092147-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1155
ID ADB31084 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003096386-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1156
ID ADA61012 standard; protein; 1119 AA.
DE Homo sapiens.
PN US2003049817-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1157
ID ADB24159 standard; protein; 1119 AA.
DE Human PRO polypeptide SEQ ID NO 352.
PN US2003077714-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1158
ID ADA96488 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.

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PN US2003082690-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1159
ID ADA81060 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003082702-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1160
ID ADA95936 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003082759-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1161
ID ADB26245 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003082760-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1162
ID ADB21730 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003082765-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1163
ID ADA77509 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003068797-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1164
ID ADB18249 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003077710-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1165
ID ADA86932 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003082709-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1166
ID ADA16754 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein, #56.
PN US2003039969-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1167
ID ADA13183 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein, #56.
PN US2003049622-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1168
ID ADA42051 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein, #56.
PN US2003082540-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1169
ID ADA98035 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003082700-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1170
ID ADA46423 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003054516-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1171
ID ADA17398 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein, #56.
PN US2003017498-A1.
PD 23-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1172
ID ADA42901 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein, #56.
PN US2003054351-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1173
ID ADB28453 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003082699-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1174
ID ADB29005 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003082706-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1175
ID ADA76957 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003059909-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1176
ID ADA88587 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003073213-A1.
PD 17-APR-2003.
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PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1177
ID ADA97592 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003082686-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1178
ID ADB27349 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003022239-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1179
ID ADB22282 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003087344-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1180
ID ABO17606 standard; protein; 1119 AA.
DE Human PRO polypeptide #52.
PN US2003064923-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1181
ID ADA66973 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003068793-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1182
ID ADB22834 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US200307711-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1183
ID ADB23607 standard; protein; 1119 AA.
DE Human PRO polypeptide SEQ ID NO 352.
PN US200307712-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1184
ID ADA92329 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003082712-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1185
ID ADB15392 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003087352-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;

RESULT 1186
ID ADB38644 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003082766-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1187
ID ADB38092 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003087347-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1188
ID ADB66564 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003082689-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1189
ID ADB89644 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003082698-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1190
ID ADB90376 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003082762-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1191
ID ADB77820 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein, #56.
PN US2003077654-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1192
ID ADB39477 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003082764-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1193
ID ADB74956 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein, #56.
PN US2003082542-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1194
ID ADB47100 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003082687-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1195

ID ADB86707 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003082697-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1196
ID ADB77312 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003082696-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1197
ID ADB34469 standard; protein; 1119 AA.
DE Human PRO polypeptide SEQ ID NO 352.
PN US2003077717-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1198
ID ADB35573 standard; protein; 1119 AA.
DE Human PRO polypeptide SEQ ID NO 352.
PN US2003077719-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1199
ID ADB33917 standard; protein; 1119 AA.
DE Human PRO polypeptide SEQ ID NO 352.
PN US2003077716-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1200
ID ADB35021 standard; protein; 1119 AA.
DE Human PRO polypeptide SEQ ID NO 352.
PN US2003077718-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1201
ID ADB36125 standard; protein; 1119 AA.
DE Human PRO polypeptide SEQ ID NO 352.
PN US2003077720-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1202
ID ADB46520 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003082692-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1203
ID ADC28602 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein, #56.
PN US2003059772-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1204
ID ADC39802 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein, #56.
PN US2003059828-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1205
ID ADC40316 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein, #56.
PN US2003059829-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1206
ID ADC19140 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein, #56.
PN US2003036061-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1207
ID ADC34440 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein, #56.
PN US2003036094-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1208
ID ADC29495 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein, #56.
PN US2003049676-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1209
ID ADC29026 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein, #56.
PN US2003049677-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1210
ID ADC40911 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein, #56.
PN US2003054400-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1211
ID ADC19568 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein, #56.
PN US2003054441-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1212
ID ADC34016 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein, #56.
PN US2003073077-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1213
ID ADC13086 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein, #56.

PD US2003073079-A1.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1214
ID ADC50393 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003092106-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1215
ID ADC71940 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003092107-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1216
ID ADC59919 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003092105-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1217
ID ADC52926 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein Seq ID352.
PN US2003087365-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1218
ID ADC57280 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein Seq ID352.
PN US2003087366-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1219
ID ADC60471 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003087367-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1220
ID ADC50946 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003087361-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1221
ID ADC65473 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003087362-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1222
ID ADC54571 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein Seq ID352.
PN US2003087363-A1.

PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1223
ID ADC53532 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein Seq ID352.
PN US2003087364-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1224
ID ADC59055 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein Seq ID352.
PN US2003087359-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1225
ID ADC55933 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein Seq ID352.
PN US2003087360-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1226
ID ADC58503 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein Seq ID352.
PN US2003087346-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1227
ID ADC12538 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein, #56.
PN US2003082541-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1228
ID ADD03177 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003092104-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1229
ID ADC90169 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003087348-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1230
ID ADC69588 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003194770-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1231
ID ADC48477 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003194773-A1.
PD 16-OCT-2003.

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PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1232
ID ADD10006 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003194776-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1233
ID ADD04581 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003087354-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1234
ID ADC80537 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003092103-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1235
ID ADD11044 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003194774-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1236
ID ADC47925 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003194771-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1237
ID ADD05093 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein, #56.
PN US2003104469-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1238
ID ADC79985 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003087358-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1239
ID ADD0454 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003194775-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1240
ID ADD04099 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein, #56.
PN US2003104381-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1241
ID ADD03675 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein, #56.
PN US2003108983-A1.
PD 12-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1242
ID ADD41167 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003203438-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1243
ID ADD52306 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003194769-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1244
ID ADD53046 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003194792-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1245
ID ADD53598 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003203437-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1246
ID ADD51754 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003194779-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1247
ID ADD02553 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003203431-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1248
ID ADD01987 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003203430-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1249
ID ADD54169 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003203432-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
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Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1250
ID ADE32486 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003199030-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1251
ID ADE31382 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003199055-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1252
ID ADE031996 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003199057-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1253
ID ADE32293 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003194765-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1254
ID ADE22225 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003199056-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1255
ID ADE79449 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003203428-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1256
ID ADE41985 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003194772-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1257
ID ADE17802 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003199023-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1258
ID ADE31934 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003199053-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;

RESULT 1259
ID ADE33397 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003194767-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1260
ID ADE33949 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003194791-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1261
ID ADE80001 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003207417-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1262
ID ADE33038 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003194768-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1263
ID ADE19458 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003199025-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1264
ID ADE34927 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein, #56.
PN US2003077583-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1265
ID ADE18906 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003199026-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1266
ID ADE43102 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003199033-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1267
ID ADE95891 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003199059-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1268
ID ADE33397 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003194767-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.

ID ADE22777 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003199064-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1269
ID AD78895 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003203429-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1270
ID ADE32845 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003194766-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1271
ID ADE42537 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003199032-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1272
ID AD80553 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003207418-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1273
ID AD89581 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003199028-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1274
ID ADE40865 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003199031-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1275
ID ADE04664 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003199034-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1276
ID ADE92793 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003194777-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1277
ID ADG21502 standard; protein; 1119 AA.

DE Novel human secreted and transmembrane protein PRO326.
PN US2003207355-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1278
ID ADG23143 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003207384-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1279
ID ADF97478 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003207370-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1280
ID ADG80542 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003207373-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1281
ID ADG79990 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003207372-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1282
ID ADH59410 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein, #56.
PN US2003039972-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1283
ID ADH55282 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003207381-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1284
ID ADH55834 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003207379-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1285
ID ADI38189 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein, #56.
PN US2003054352-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1286
ID ADI64053 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.

PD US2003207385-A1.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1287
ID ADI65002 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003207386-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1288
ID ADI63501 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003207387-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1289
ID ADH81915 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003207388-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1290
ID ADH81363 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003207377-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1291
ID ADJ26457 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein, #56.
PN US2003054349-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1292
ID ADM82532 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003087355-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1293
ID ADNI5931 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003087353-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1294
ID ADNI6560 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003087385-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1295
ID ADNI5379 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003087356-A1.

PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1296
ID ADNI4827 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003087357-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1297
ID ADC81089 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003092115-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1298
ID ADE79372 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein, #56.
PN US2003135025-A1.
PD 17-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1299
ID ADD76537 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003100087-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1300
ID ADD87901 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003092113-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1301
ID ADD86305 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003203440-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1302
ID ADE79796 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein, #56.
PN US2003130489-A1.
PD 10-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1303
ID ADE75753 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003211571-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1304
ID ADE73472 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein, #56.
PN US2003129592-A1.
PD 10-JUL-2003.

[illegible]

Query Match	12.4%;	Score 224;	DB 8;	Length 1119;
Best Local Similarity	23.9%;	Pred. No. 7.5e-10;		
RESULT 1314				
ID ADE94683 standard; protein;	1119 AA.			
DE Human PRO polypeptide #176.				
FN US2003199027-A1.				
PD 23-OCT-2003.				
PA (GETH) GENENTECH INC.				
Query Match	12.4%;	Score 224;	DB 8;	Length 1119;
Best Local Similarity	23.9%;	Pred. No. 7.5e-10;		
RESULT 1315				
ID ABE91094 standard; protein;	1119 AA.			
DE Human PRO polypeptide #176.				
FN US2003199061-A1.				
PD 23-OCT-2003.				
PA (GETH) GENENTECH INC.				
Query Match	12.4%;	Score 224;	DB 8;	Length 1119;
Best Local Similarity	23.9%;	Pred. No. 7.5e-10;		
RESULT 1316				
ID ADE95235 standard; protein;	1119 AA.			
DE Human PRO polypeptide #176.				
FN US2003199052-A1.				
PD 23-OCT-2003.				
PA (GETH) GENENTECH INC.				
Query Match	12.4%;	Score 224;	DB 8;	Length 1119;
Best Local Similarity	23.9%;	Pred. No. 7.5e-10;		
RESULT 1317				
ID ADE93345 standard; protein;	1119 AA.			
DE Human PRO polypeptide #176.				
FN US2003199060-A1.				
PD 23-OCT-2003.				
PA (GETH) GENENTECH INC.				
Query Match	12.4%;	Score 224;	DB 8;	Length 1119;
Best Local Similarity	23.9%;	Pred. No. 7.5e-10;		
RESULT 1318				
ID ADF34926 standard; protein;	1119 AA.			
DE Human PRO polypeptide #176.				
FN US2003199029-A1.				
PD 23-OCT-2003.				
PA (GETH) GENENTECH INC.				
Query Match	12.4%;	Score 224;	DB 8;	Length 1119;
Best Local Similarity	23.9%;	Pred. No. 7.5e-10;		
RESULT 1319				
ID ADE98680 standard; protein;	1119 AA.			
DE Human secreted/transmembrane protein, #56.				
FN US2003211569-A1.				
PD 13-NOV-2003.				
PA (GETH) GENENTECH INC.				
Query Match	12.4%;	Score 224;	DB 8;	Length 1119;
Best Local Similarity	23.9%;	Pred. No. 7.5e-10;		
RESULT 1320				
ID ADE92441 standard; protein;	1119 AA.			
DE Novel human secreted and transmembrane protein PRO326.				
FN US2003199051-A1.				
PD 23-OCT-2003.				
PA (GETH) GENENTECH INC.				
Query Match	12.4%;	Score 224;	DB 8;	Length 1119;
Best Local Similarity	23.9%;	Pred. No. 7.5e-10;		
RESULT 1321				
ID ADE90542 standard; protein;	1119 AA.			
DE Human PRO polypeptide #176.				
FN US2003199063-A1.				
PD 23-OCT-2003.				
PA (GETH) GENENTECH INC.				
Query Match	12.4%;	Score 224;	DB 8;	Length 1119;
Best Local Similarity	23.9%;	Pred. No. 7.5e-10;		
RESULT 1322				
ID ADE91689 standard; protein;	1119 AA.			
DE Novel human secreted and transmembrane protein PRO326.				
FN US2003199058-A1.				
PD 23-OCT-2003.				
PA (GETH) GENENTECH INC.				
Query Match	12.4%;	Score 224;	DB 8;	Length 1119;
Best Local Similarity	23.9%;	Pred. No. 7.5e-10;		
RESULT 1323				
ID ADE91689 standard; protein;	1119 AA.			
DE Novel human secreted and transmembrane protein PRO326.				
FN US2003199058-A1.				
PD 23-OCT-2003.				
PA (GETH) GENENTECH INC.				
Query Match	12.4%;	Score 224;	DB 8;	Length 1119;
Best Local Similarity	23.9%;	Pred. No. 7.5e-10;		
RESULT 1324				
ID ADE91689 standard; protein;	1119 AA.			
DE Novel human secreted and transmembrane protein PRO326.				
FN US2003199058-A1.				
PD 23-OCT-2003.				
PA (GETH) GENENTECH INC.				
Query Match	12.4%;	Score 224;	DB 8;	Length 1119;
Best Local Similarity	23.9%;	Pred. No. 7.5e-10;		
RESULT 1325				
ID ADE91689 standard; protein;	1119 AA.			
DE Novel human secreted and transmembrane protein PRO326.				
FN US2003199058-A1.				
PD 23-OCT-2003.				
PA (GETH) GENENTECH INC.				
Query Match	12.4%;	Score 224;	DB 8;	Length 1119;
Best Local Similarity	23.9%;	Pred. No. 7.5e-10;		
RESULT 1326				
ID ADE91689 standard; protein;	1119 AA.			
DE Novel human secreted and transmembrane protein PRO326.				
FN US2003199058-A1.				
PD 23-OCT-2003.				
PA (GETH) GENENTECH INC.				

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Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1323
ID ADE99107 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein, #56.
PN US20032111568-A1.
PD 13-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1324
ID ADG40577 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein, #56.
PN US2003225253-A1.
PD 04-DEC-2003.
PA (DESN/) DESNOYERS L.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (MATH/) MATHIER J P.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1325
ID ADF73971 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein, #56.
PN US2003180312-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1326
ID ADG02268 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003207352-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1327
ID ADG22054 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003207360-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1328
ID ADG20124 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003207376-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1329
ID ADF98030 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003207422-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1330
ID ADG24247 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003207426-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1331
ID ADF98601 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003208055-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1332
ID ADG03432 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003207351-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1333
ID ADF99153 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003207353-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1334
ID ADG16738 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003207359-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1335
ID ADG05197 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003207375-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1336
ID ADG19464 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003207425-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1337
ID ADF73547 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein, #56.
PN US2003166051-A1.
PD 04-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1338
ID ADG13301 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003207357-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1339
ID ADG08358 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003207424-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1340
ID ADG15528 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
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PN US2003219885-A1.
PD 27-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1341
ID ADF96926 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003207371-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1342
ID ADG06111 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003207374-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1343
ID ADG23695 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003207389-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1344
ID ADG03984 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003207423-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1345
ID ADG24885 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003207427-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1346
ID ADG07182 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003207350-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1347
ID ADG07734 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003207356-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1348
ID ADG55229 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003194778-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1349
ID ADG60893 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003207390-A1.

PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1350
ID ADG61997 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003207428-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1351
ID ADG92390 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein, #56.
PN US2003027145-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1352
ID ADG82198 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003207358-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1353
ID ADG57437 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003207362-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1354
ID ADG56885 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003207364-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1355
ID ADG55781 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003207365-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1356
ID ADG58541 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003207368-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1357
ID ADG70907 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003207420-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1358
ID ADG92817 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein, #56.
PN US2003027146-A1.
PD 06-FEB-2003.

PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1359
ID ADG57989 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003207363-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1360
ID ADG53573 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003207415-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1361
ID ADG71459 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003207421-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1362
ID ADG81646 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003207805-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1363
ID ADH30608 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US200307723-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1364
ID ADH11975 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003207419-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1365
ID ADG52397 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003207414-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1366
ID ADG54125 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003207416-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1367
ID ADG81094 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003194793-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;

Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1368
ID ADG56333 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003207366-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1369
ID ADH12599 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003207378-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1370
ID ADG61445 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003207429-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1371
ID ADH28532 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003022331-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1372
ID ADG54677 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003207367-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1373
ID ADG59717 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003207369-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1374
ID ADH20606 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein, #56.
PN US2004005553-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1375
ID ADH07461 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein, #56.
PN US2004006211-A1.
PD 08-JAN-2004.
PA (DESN)/ DESNOYERS L.
PA (GODD)/ GODDARD A.
PA (GODO)/ GODOWSKI P J.
PA (GURN)/ GURNEY A L.
PA (MATH)/ MATHER J P.
PA (WILL)/ WILLIAMS P M.
PA (WOOD)/ WOOD W I.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.5e-10;
RESULT 1376
ID ADH60006 standard; protein; 1119 AA.

DE Human secreted/transmembrane protein, #56.
 PN US2003215904-A1.
 PD 20-NOV-2003.
 PA (GETH) GENENTECH INC.
 Query Match 12.4%; Score 224; DB 8; Length 1119;
 Best Local Similarity 23.9%; Pred. No. 7.5e-10;
 RESULT 1377
 ID ADH07034 standard; protein; 1119 AA.
 DE Human secreted/transmembrane protein, #56.
 PN US2004005665-A1.
 PD 08-JAN-2004.
 PA (DESN/) DESNOYERS L.
 PA (GODD/) GODDARD A.
 PA (GODO/) GODOWSKI P J.
 PA (GURN/) GURNEY A L.
 PA (MATH/) MATHER J P.
 PA (WILL/) WILLIAMS P M.
 PA (WOOD/) WOOD W I.
 Query Match 12.4%; Score 224; DB 8; Length 1119;
 Best Local Similarity 23.9%; Pred. No. 7.5e-10;
 RESULT 1378
 ID AD181141 standard; protein; 1119 AA.
 DE Human PRO polypeptide #176.
 PN US2003207361-A1.
 PD 06-NOV-2003.
 PA (GETH) GENENTECH INC.
 Query Match 12.4%; Score 224; DB 8; Length 1119;
 Best Local Similarity 23.9%; Pred. No. 7.5e-10;
 RESULT 1379
 ID AD118776 standard; protein; 1119 AA.
 DE Human secreted/transmembrane protein, #56.
 PN US2003152999-A1.
 PD 14-AUG-2003.
 PA (GETH) GENENTECH INC.
 Query Match 12.4%; Score 224; DB 8; Length 1119;
 Best Local Similarity 23.9%; Pred. No. 7.5e-10;
 RESULT 1380
 ID AD137755 standard; protein; 1119 AA.
 DE Human secreted/transmembrane protein, #56.
 PN US2003096340-A1.
 PD 22-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 12.4%; Score 224; DB 8; Length 1119;
 Best Local Similarity 23.9%; Pred. No. 7.5e-10;
 RESULT 1381
 ID ADG09884 standard; protein; 1119 AA.
 DE Novel human secreted and transmembrane protein PRO326.
 PN US2004009548-A1.
 PD 15-JAN-2004.
 PA (GETH) GENENTECH INC.
 Query Match 12.4%; Score 224; DB 8; Length 1119;
 Best Local Similarity 23.9%; Pred. No. 7.5e-10;
 RESULT 1382
 ID ADH97555 standard; protein; 1119 AA.
 DE Human secreted/transmembrane protein, #56.
 PN US2003190610-A1.
 PD 09-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 12.4%; Score 224; DB 8; Length 1119;
 Best Local Similarity 23.9%; Pred. No. 7.5e-10;
 RESULT 1383
 ID AD115355 standard; protein; 1119 AA.
 DE Novel human secreted and transmembrane protein PRO326.
 PN US2003207382-A1.
 PD 06-NOV-2003.
 PA (GETH) GENENTECH INC.
 Query Match 12.4%; Score 224; DB 8; Length 1119;
 Best Local Similarity 23.9%; Pred. No. 7.5e-10;
 RESULT 1384
 ID ADG09232 standard; protein; 1119 AA.
 DE Novel human secreted and transmembrane protein PRO326.
 PN US2004009547-A1.
 PD 15-JAN-2004.
 PA (GETH) GENENTECH INC.
 Query Match 12.4%; Score 224; DB 8; Length 1119;
 Best Local Similarity 23.9%; Pred. No. 7.5e-10;
 RESULT 1385
 ID ADI65923 standard; protein; 1119 AA.
 DE Human secreted/transmembrane protein, #56.
 PN US2003148371-A1.
 PD 07-AUG-2003.
 PA (GETH) GENENTECH INC.
 Query Match 12.4%; Score 224; DB 8; Length 1119;
 Best Local Similarity 23.9%; Pred. No. 7.5e-10;
 RESULT 1386
 ID ADI14687 standard; protein; 1119 AA.
 DE Novel human secreted and transmembrane protein PRO326.
 PN US2003207383-A1.
 PD 06-NOV-2003.
 PA (GETH) GENENTECH INC.
 Query Match 12.4%; Score 224; DB 8; Length 1119;
 Best Local Similarity 23.9%; Pred. No. 7.5e-10;
 RESULT 1387
 ID ADH60666 standard; protein; 1119 AA.
 DE Human secreted/transmembrane protein, #56.
 PN US2004023331-A1.
 PD 05-FEB-2004.
 PA (DESN/) DESNOYERS L.
 PA (GODD/) GODDARD A.
 PA (GODO/) GODOWSKI P J.
 PA (GURN/) GURNEY A L.
 PA (MATH/) MATHER J P.
 PA (WILL/) WILLIAMS P M.
 PA (WOOD/) WOOD W I.
 Query Match 12.4%; Score 224; DB 8; Length 1119;
 Best Local Similarity 23.9%; Pred. No. 7.5e-10;
 RESULT 1388
 ID ADI18282 standard; protein; 1119 AA.
 DE Novel human secreted and transmembrane protein PRO326.
 PN US2003207349-A1.
 PD 06-NOV-2003.
 PA (GETH) GENENTECH INC.
 Query Match 12.4%; Score 224; DB 8; Length 1119;
 Best Local Similarity 23.9%; Pred. No. 7.5e-10;
 RESULT 1389
 ID ADJ9723 standard; protein; 1119 AA.
 DE Human secreted/transmembrane protein, #56.
 PN US2003187238-A1.
 PD 02-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 12.4%; Score 224; DB 8; Length 1119;
 Best Local Similarity 23.9%; Pred. No. 7.5e-10;
 RESULT 1390
 ID ADL08916 standard; protein; 1119 AA.
 DE Human secreted/transmembrane protein, #56.
 PN US2003186358-A1.
 PD 02-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 12.4%; Score 224; DB 8; Length 1119;
 Best Local Similarity 23.9%; Pred. No. 7.5e-10;
 RESULT 1391
 ID ADM25257 standard; protein; 1119 AA.
 DE Human secreted/transmembrane protein, #56.
 PN US2003096233-A1.
 PD 22-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 12.4%; Score 224; DB 8; Length 1119;
 Best Local Similarity 23.9%; Pred. No. 7.5e-10;
 RESULT 1392
 ID ADJ63563 standard; protein; 1119 AA.
 DE Novel human secreted and transmembrane protein PRO326.
 PN US2004039164-A1.
 PD 26-FEB-2004.
 PA (GETH) GENENTECH INC.
 Query Match 12.4%; Score 224; DB 8; Length 1119;
 Best Local Similarity 23.9%; Pred. No. 7.5e-10;

RESULT 1393
 ID ADM30007 standard; protein; 1119 AA.
 DE Human secreted/transmembrane protein, #56.
 PN US2003190611-A1.
 PD 09-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 12.4%; Score 224; DB 8; Length 1119;
 Best Local Similarity 23.9%; Pred. No. 7.5e-10;
 RESULT 1394
 ID ADJ77458 standard; protein; 1119 AA.
 DE Human PRO polypeptide #176.
 PN US2004038336-A1.
 PD 26-FEB-2004.
 PA (GETH) GENENTECH INC.
 Query Match 12.4%; Score 224; DB 8; Length 1119;
 Best Local Similarity 23.9%; Pred. No. 7.5e-10;
 RESULT 1395
 ID ADJ65580 standard; protein; 1119 AA.
 DE Human PRO polypeptide #176.
 PN US2004038335-A1.
 PD 26-FEB-2004.
 PA (GETH) GENENTECH INC.
 Query Match 12.4%; Score 224; DB 8; Length 1119;
 Best Local Similarity 23.9%; Pred. No. 7.5e-10;
 RESULT 1396
 ID ADM27716 standard; protein; 1119 AA.
 DE Human PRO polypeptide #176.
 PN US2004048333-A1.
 PD 11-MAR-2004.
 PA (GETH) GENENTECH INC.
 Query Match 12.4%; Score 224; DB 8; Length 1119;
 Best Local Similarity 23.9%; Pred. No. 7.5e-10;
 RESULT 1397
 ID ADM42440 standard; protein; 1119 AA.
 DE Human PRO polypeptide #176.
 PN US2004058424-A1.
 PD 25-MAR-2004.
 PA (GETH) GENENTECH INC.
 Query Match 12.4%; Score 224; DB 8; Length 1119;
 Best Local Similarity 23.9%; Pred. No. 7.5e-10;
 RESULT 1398
 ID ADO06329 standard; protein; 1119 AA.
 DE Human PRO polypeptide #52.
 PN US6686451-B1.
 PD 03-FEB-2004.
 PA (GETH) GENENTECH INC.
 Query Match 12.4%; Score 224; DB 8; Length 1119;
 Best Local Similarity 23.9%; Pred. No. 7.5e-10;
 RESULT 1399
 ID ADM28302 standard; protein; 1119 AA.
 DE Human PRO polypeptide #176.
 PN US2004077064-A1.
 PD 22-APR-2004.
 PA (GETH) GENENTECH INC.
 Query Match 12.4%; Score 224; DB 8; Length 1119;
 Best Local Similarity 23.9%; Pred. No. 7.5e-10;
 RESULT 1400
 ID ADR11181 standard; protein; 1119 AA.
 DE Human secreted/transmembrane protein, #56.
 PN US2004137561-A1.
 PD 15-JUL-2004.
 PA (GETH) GENENTECH INC.
 Query Match 12.4%; Score 224; DB 8; Length 1119;
 Best Local Similarity 23.9%; Pred. No. 7.5e-10;
 RESULT 1401
 ID ADR18090 standard; protein; 1119 AA.
 DE Human secreted/transmembrane protein, #56.
 PN US2004147017-A1.
 PD 29-JUL-2004.
 PA (ASHK/) ASHKENAZI A.
 PA (BOTS/) BOTSTEIN D.
 PA (DESN/) DESNOYERS L.
 PA (EATO/) EATON D L.

PA (FERR/) FERRARA N.
 PA (FILV/) FILVAROFF E.
 PA (FONG/) FONG S.
 PA (GROW/) GAO W.
 PA (GERB/) GERBER H.
 PA (GERR/) GERRITSEN M E.
 PA (GODD/) GODDARD A.
 PA (GODO/) GODOWSKI P J.
 PA (GRIM/) GRIMALDI C J.
 PA (GURN/) GURNEY A L.
 PA (HILL/) HILLAN K J.
 PA (KLJA/) KLJAVIN I J.
 PA (MATH/) MATHER J P.
 PA (PANJ/) PAN J.
 PA (PAON/) PAONI N F.
 PA (ROYM/) ROY M A.
 PA (STEW/) STEWART T A.
 PA (TUMA/) TUMAS D.
 PA (WILL/) WILLIAMS P M.
 PA (WOOD/) WOOD W I.
 Query Match 12.4%; Score 224; DB 8; Length 1119;
 Best Local Similarity 23.9%; Pred. No. 7.5e-10;
 RESULT 1402
 ID ADI95784 standard; protein; 1119 AA.
 DE Human PRO polypeptide #176.
 PN US2003077659-A1.
 PD 24-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 12.4%; Score 224; DB 8; Length 1119;
 Best Local Similarity 23.9%; Pred. No. 7.5e-10;
 RESULT 1403
 ID ADI96336 standard; protein; 1119 AA.
 DE Novel human secreted and transmembrane protein PRO326.
 PN US2003207354-A1.
 PD 06-NOV-2003.
 PA (GETH) GENENTECH INC.
 Query Match 12.4%; Score 224; DB 8; Length 1119;
 Best Local Similarity 23.9%; Pred. No. 7.5e-10;
 RESULT 1404
 ID ADS74729 standard; protein; 1119 AA.
 DE Human secreted/transmembrane protein #56.
 PN US2004185531-A1.
 PD 23-SEP-2004.
 PA (ASHK/) ASHKENAZI A.
 PA (BOTS/) BOTSTEIN D.
 PA (DESN/) DESNOYERS L.
 PA (EATO/) EATON D L.
 PA (FERR/) FERRARA N.
 PA (FILV/) FILVAROFF E.
 PA (FONG/) FONG S.
 PA (GROW/) GAO W.
 PA (GERB/) GERBER H.
 PA (GERR/) GERRITSEN M E.
 PA (GODD/) GODDARD A.
 PA (GODO/) GODOWSKI P J.
 PA (GRIM/) GRIMALDI C J.
 PA (GURN/) GURNEY A L.
 PA (HILL/) HILLAN K J.
 PA (KLJA/) KLJAVIN I J.
 PA (MATH/) MATHER J P.
 PA (PANJ/) PAN J.
 PA (PAON/) PAONI N F.
 PA (ROYM/) ROY M A.
 PA (STEW/) STEWART T A.
 PA (TUMA/) TUMAS D.
 PA (WILL/) WILLIAMS P M.
 PA (WOOD/) WOOD W I.
 Query Match 12.4%; Score 224; DB 8; Length 1119;
 Best Local Similarity 23.9%; Pred. No. 7.5e-10;
 RESULT 1405
 ID ADS32288 standard; protein; 1119 AA.
 DE Novel human secreted and transmembrane protein PRO326.
 PN US2004203125-A1.

PD 14-OCT-2004.
 PA (GETH) GENENTECH INC.
 Query Match 12.4%; Score 224; DB 8; Length 1119;
 Best Local Similarity 23.9%; Pred. No. 7.5e-10;
 RESULT 1406
 ID AD703272 standard; protein; 1119 AA.
 DE Human PRO polypeptide #176.
 PN US2004214269-A1.
 PD 28-OCT-2004.
 PA (GETH) GENENTECH INC.
 Query Match 12.4%; Score 224; DB 8; Length 1119;
 Best Local Similarity 23.9%; Pred. No. 7.5e-10;
 RESULT 1407
 ID AD703766 standard; protein; 1119 AA.
 DE Human secreted/transmembrane protein, #56.
 PN US2003152922-A1.
 PD 14-AUG-2003.
 PA (GETH) GENENTECH INC.
 Query Match 12.4%; Score 224; DB 8; Length 1119;
 Best Local Similarity 23.9%; Pred. No. 7.5e-10;
 RESULT 1408
 ID AD203323 standard; protein; 1119 AA.
 DE Human secreted/transmembrane PRO326 protein.
 PN US2005074837-A1.
 PD 07-APR-2005.
 PA (GETH) GENENTECH INC.
 Query Match 12.4%; Score 224; DB 9; Length 1119;
 Best Local Similarity 23.9%; Pred. No. 7.5e-10;
 RESULT 1409
 ID AEA38004 standard; protein; 1119 AA.
 DE Human secreted/transmembrane protein, #56.
 PN US2005112725-A1.
 PD 26-MAY-2005.
 PA (GETH) GENENTECH INC.
 Query Match 12.4%; Score 224; DB 9; Length 1119;
 Best Local Similarity 23.9%; Pred. No. 7.5e-10;
 RESULT 1410
 ID AEB14069 standard; protein; 1119 AA.
 DE Cancer cell diagnosis method-related human protein - SEQ ID 352.
 PN US2005153396-A1.
 PD 14-JUL-2005.
 PA (BAKE/) BAKER K P.
 PA (BERE/) BRESINI M.
 PA (DEFO/) DEFORGE L.
 PA (DESN/) DESNOYERS L.
 PA (FILV/) FILVAROFF E.
 PA (GAOW/) GAO W.
 PA (GERR/) GERRITSEN M E.
 PA (GODD/) GODDARD A.
 PA (GODO/) GODOWSKI P J.
 PA (GURN/) GURNEY A L.
 PA (SHER/) SHERWOOD S.
 PA (SMIT/) SMITH V.
 PA (STEW/) STEWART T A.
 PA (TUMA/) TUMAS D.
 PA (WATA/) WATANABE C K.
 PA (WOOD/) WOOD W I.
 PA (ZHAN/) ZHANG Z.
 Query Match 12.4%; Score 224; DB 9; Length 1119;
 Best Local Similarity 23.9%; Pred. No. 7.5e-10;
 RESULT 1411
 ID AED24038 standard; protein; 1119 AA.
 DE Human secreted protein PRO 326, SEQ ID 294.
 PN US2005214904-A1.
 PD 29-SEP-2005.
 PA (GETH) GENENTECH INC.
 Query Match 12.4%; Score 224; DB 9; Length 1119;
 Best Local Similarity 23.9%; Pred. No. 7.5e-10;
 RESULT 1412
 ID AED86267 standard; protein; 1119 AA.
 DE Human PRO amino acid sequence, seq id 352.
 PN US2005245730-A1.
 PD 03-NOV-2005.

PA (GETH) GENENTECH INC.
 Query Match 12.4%; Score 224; DB 9; Length 1119;
 Best Local Similarity 23.9%; Pred. No. 7.5e-10;
 RESULT 1413
 ID ABE69207 standard; protein; 1119 AA.
 DE Leucine rich repeat protein homologous PRO326 protein, SEQ ID 294.
 PN US6974689-B1.
 PD 13-DEC-2005.
 PA (GETH) GENENTECH INC.
 Query Match 12.4%; Score 224; DB 10; Length 1119;
 Best Local Similarity 23.9%; Pred. No. 7.5e-10;
 RESULT 1414
 ID ADA55073 standard; protein; 1251 AA.
 DE Human protein, SEQ ID 2641.
 PN EP1293569-A2.
 PD 19-MAR-2003.
 PA (HELI-) HELIX RES INST.
 PA (REAS-) RES ASSOC BIOTECHNOLOGY.
 Query Match 12.4%; Score 224; DB 6; Length 1251;
 Best Local Similarity 25.9%; Pred. No. 8.8e-10;
 RESULT 1415
 ID ABU11674 standard; protein; 380 AA.
 DE Human MDDT polypeptide SEQ ID 621.
 PN WO200279449-A2.
 PD 10-OCT-2002.
 PA (INCY-) INCYTE GENOMICS INC.
 Query Match 12.3%; Score 223; DB 6; Length 380;
 Best Local Similarity 26.4%; Pred. No. 2.1e-10;
 RESULT 1416
 ID AAY53028 standard; protein; 414 AA.
 DE Human secreted protein clone cw1000_2 protein sequence SEQ ID NO:62.
 PN WO9957132-A1.
 PD 11-NOV-1999.
 PA (GEMY) GENETICS INST INC.
 Query Match 12.3%; Score 223; DB 3; Length 414;
 Best Local Similarity 24.9%; Pred. No. 2.4e-10;
 RESULT 1417
 ID ABJ20228 standard; protein; 798 AA.
 DE Human IG gene related protein SEQ ID No 51.
 PN WO20029040-A2.
 PD 12-DEC-2002.
 PA (EXEL-) EXELIXIS INC.
 Query Match 12.3%; Score 223; DB 6; Length 798;
 Best Local Similarity 24.8%; Pred. No. 5.8e-10;
 RESULT 1418
 ID ABB97578 standard; protein; 1179 AA.
 DE Novel human protein SEQ ID NO: 846.
 PN WO200222660-A2.
 PD 21-MAR-2002.
 PA (HYSE-) HYSEQ INC.
 Query Match 12.3%; Score 223; DB 5; Length 1179;
 Best Local Similarity 24.8%; Pred. No. 9.9e-10;
 RESULT 1419
 ID ADR28014 standard; protein; 1179 AA.
 DE Long form IGSF9 protein.
 PN WO2004066933-A2.
 PD 12-AUG-2004.
 PA (MCLA/) MCLACHLAN K.
 PA (GLAS/) GLASER S.
 PA (PEAC/) PEACH R J.
 PA (ROWE/) ROWE T.
 Query Match 12.3%; Score 223; DB 8; Length 1179;
 Best Local Similarity 24.8%; Pred. No. 9.9e-10;
 RESULT 1420
 ID ADR28013 standard; protein; 1179 AA.
 DE Long form full-length IGSF9 protein.
 PN WO2004066933-A2.
 PD 12-AUG-2004.
 PA (MCLA/) MCLACHLAN K.
 PA (GLAS/) GLASER S.
 PA (PEAC/) PEACH R J.
 PA (ROWE/) ROWE T.
 Query Match 12.3%; Score 223; DB 8; Length 1179;

Best Local Similarity 24.8%; Pred. No. 9.9e-10;
RESULT 1421
ID ADR09753 standard; protein; 595 AA.
DE Human protein useful for treating neurological disease Seq 3259.
PN EPI447413-A2.
PD 18-AUG-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match
Best Local Similarity 12.3%; Score 222; DB 8; Length 595;
PD 27.2%; Pred. No. 4.7e-10;
RESULT 1422
ID ABB10202 standard; protein; 744 AA.
DE Human CDNA SEQ ID NO: 510.
PN WO200154474-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 12.3%; Score 222; DB 4; Length 744;
PD 23.6%; Pred. No. 6.4e-10;
RESULT 1423
ID ABP66789 standard; protein; 744 AA.
DE Human polypeptide SEQ ID NO 510.
PN US2002090672-A1.
PD 11-JUL-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match
Best Local Similarity 12.3%; Score 222; DB 5; Length 744;
PD 23.6%; Pred. No. 6.4e-10;
RESULT 1424
ID ADH72194 standard; protein; 1068 AA.
DE Human protein of the invention NOV51d SEQ ID NO:1090.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match
Best Local Similarity 12.3%; Score 222; DB 8; Length 1068;
PD 24.2%; Pred. No. 1.1e-09;
RESULT 1425
ID AEC79581 standard; protein; 733 AA.
DE Human PTK7 CDNA cluster T51958, protein T51958_PEA_1_P5.
PN WO2005072053-A2.
PD 11-AUG-2005.
PA (COMP-) COMPUGEN LTD.
Query Match
Best Local Similarity 12.3%; Score 221.5; DB 9; Length 733;
PD 26.3%; Pred. No. 6.9e-10;
RESULT 1426
ID AAW42087 standard; protein; 1571 AA.
DE Human Down syndrome-cell adhesion molecule DS-CAM2.
PN WO9817795-A1.
PD 30-APR-1998.
PA (CEDA-) CEDARS SINAI MEDICAL CENT.
Query Match
Best Local Similarity 12.2%; Score 221; DB 2; Length 1571;
PD 28.6%; Pred. No. 2.2e-09;
RESULT 1427
ID AAW42086 standard; protein; 1910 AA.
DE Human Down syndrome-cell adhesion molecule DS-CAM1.
PN WO9817795-A1.
PD 30-APR-1998.
PA (CEDA-) CEDARS SINAI MEDICAL CENT.
Query Match
Best Local Similarity 12.2%; Score 221; DB 2; Length 1910;
PD 28.6%; Pred. No. 2.8e-09;
RESULT 1428
ID ADK71092 standard; protein; 2012 AA.
DE Human WP21 polypeptide.
PN WO2004015073-A2.
PD 19-FEB-2004.
PA (EXEL-) EXELIXIS INC.
Query Match
Best Local Similarity 12.2%; Score 221; DB 8; Length 2012;
PD 28.6%; Pred. No. 3.1e-09;
RESULT 1429
ID AAB25586 standard; protein; 364 AA.
DE Protein encoded by human secreted protein gene #11.
PN WO200029435-A1.
PD 25-MAY-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 12.2%; Score 220.5; DB 3; Length 364;
PD 26.0%; Pred. No. 3.3e-10;
RESULT 1430
ID ADA27058 standard; protein; 364 AA.
DE Human novel secreted protein from CDNA HOUJ81 #1.
PN US2003052331-A1.
PD 20-MAR-2003.
PA (NIJ/) NI J.
PA (YOUN/) YOUNG P E.
PA (KINN/) KENNY J J.
PA (OLSE/) OLSEN H S.
PA (MOOR/) MOORE P A.
PA (WEIY/) WEI Y.
PA (GREE/) GREENE J M.
PA (RUBE/) RUBEN S M.
PA (LIUD/) LIU D.
PA (CROC/) CROCKER P R.
Query Match
Best Local Similarity 12.2%; Score 220.5; DB 6; Length 364;
PD 26.0%; Pred. No. 3.3e-10;
RESULT 1431
ID AD86588 standard; protein; 364 AA.
DE Novel human secreted protein #11.
PN US2003129685-A1.
PD 10-JUL-2003.
PA (NIJ/) NI J.
PA (YOUN/) YOUNG P E.
PA (KINN/) KENNY J J.
PA (OLSE/) OLSEN H S.
PA (MOOR/) MOORE P A.
PA (WEIY/) WEI Y.
PA (GREE/) GREENE J M.
PA (RUBE/) RUBEN S M.
Query Match
Best Local Similarity 12.2%; Score 220.5; DB 8; Length 364;
PD 26.0%; Pred. No. 3.3e-10;
RESULT 1432
ID ADR41469 standard; protein; 370 AA.
DE Human CD-like molecule HATCZ07, SEQ ID NO:268.
PN WO200226930-A2.
PD 04-APR-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 12.2%; Score 220.5; DB 5; Length 370;
PD 26.0%; Pred. No. 3.3e-10;
RESULT 1433
ID AAM23691 standard; protein; 402 AA.
DE Human EST encoded protein SEQ ID NO: 1216.
PN WO200154477-A2.
PD 02-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 12.2%; Score 220.5; DB 4; Length 402;
PD 26.0%; Pred. No. 3.7e-10;
RESULT 1434
ID AA45093 standard; protein; 423 AA.
DE Mouse lymphoid derived dendritic cell adhesion molecule.
PN WO200008158-A2.
PD 17-FEB-2000.
PA (IMMV) IMMUNEX CORP.
Query Match
Best Local Similarity 12.2%; Score 220.5; DB 3; Length 423;
PD 26.0%; Pred. No. 4e-10;
RESULT 1435
ID ADW91678 standard; protein; 423 AA.
DE Mouse LDCAM.
PN WO2005012530-A2.
PD 10-FEB-2005.
PA (AMGE-) AMGEN INC.
Query Match
Best Local Similarity 12.2%; Score 220.5; DB 9; Length 423;
PD 26.0%; Pred. No. 4e-10;
RESULT 1436
ID AB084564 standard; protein; 425 AA.
DE Human cancer-associated protein HP16-039.1.
PN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match
Best Local Similarity 12.2%; Score 220.5; DB 8; Length 425;
PD 26.0%; Pred. No. 3.3e-10;

Best Local Similarity	26.0%;	Pred. No. 4e-10;	Query Match	12.2%;	Score 220.5;	DB 6;	Length 440;
RESULT 1437			Best Local Similarity	26.0%;	Pred. No. 4.2e-10;		
ID AAY17830 standard; protein; 440 AA.			RESULT 1447				
DE Human PRO355 protein sequence.			ID ABU82722 standard; protein; 440 AA.				
PN WQ9928462-A2.			DE Human PRO polypeptide #17.				
PD 10-JUN-1999.			PN US2003032113-A1.				
PA (GETH) GENENTECH INC.			PD 13-FEB-2003.				
Query Match	12.2%;	Score 220.5;	Query Match	12.2%;	Score 220.5;	DB 6;	Length 440;
Best Local Similarity	26.0%;	Pred. No. 4.2e-10;	Best Local Similarity	26.0%;	Pred. No. 4.2e-10;		
RESULT 1438			RESULT 1448				
ID AAB01321 standard; protein; 440 AA.			ID ABU89843 standard; protein; 440 AA.				
DE Human PRO355 polypeptide.			DE Novel human secreted and transmembrane protein PRO355.				
PN WO20032776-A2.			PN US2003036147-A1.				
PD 08-JUN-2000.			PD 20-FEB-2003.				
PA (GETH) GENENTECH INC.			Query Match	12.2%;	Score 220.5;	DB 6;	Length 440;
Query Match	12.2%;	Score 220.5;	Best Local Similarity	26.0%;	Pred. No. 4.2e-10;		
Best Local Similarity	26.0%;	Pred. No. 4.2e-10;	RESULT 1449				
RESULT 1439			ID ABR68092 standard; protein; 440 AA.				
ID AAU29040 standard; protein; 440 AA.			DE Human secreted polypeptide PRO355, SEQ ID NO:34.				
DE Human PRO polypeptide sequence #17.			PN US2003027264-A1.				
PN WO200168848-A2.			PD 06-FEB-2003.				
PD 20-SEP-2001.			Query Match	12.2%;	Score 220.5;	DB 6;	Length 440;
PA (GETH) GENENTECH INC.			Best Local Similarity	26.0%;	Pred. No. 4.2e-10;		
Query Match	12.2%;	Score 220.5;	RESULT 1450				
Best Local Similarity	26.0%;	Pred. No. 4.2e-10;	ID ABU96145 standard; protein; 440 AA.				
RESULT 1440			DE Novel human secreted and transmembrane protein PRO355.				
ID ABU58416 standard; protein; 440 AA.			PN US2003036144-A1.				
DE Human PRO polypeptide #17.			PD 20-FEB-2003.				
PN US2003027272-A1.			Query Match	12.2%;	Score 220.5;	DB 6;	Length 440;
PD 06-FEB-2003.			Best Local Similarity	26.0%;	Pred. No. 4.2e-10;		
PA (GETH) GENENTECH INC.			RESULT 1451				
Query Match	12.2%;	Score 220.5;	ID ABU92576 standard; protein; 440 AA.				
Best Local Similarity	26.0%;	Pred. No. 4.2e-10;	DE Human secreted/transmembrane protein (PRO) #17.				
RESULT 1441			PN US2003036149-A1.				
ID ABU87964 standard; protein; 440 AA.			PD 20-FEB-2003.				
DE Novel human secreted and transmembrane protein PRO355.			Query Match	12.2%;	Score 220.5;	DB 6;	Length 440;
PN US2003032127-A1.			Best Local Similarity	26.0%;	Pred. No. 4.2e-10;		
PD 13-FEB-2003.			RESULT 1452				
Query Match	12.2%;	Score 220.5;	ID ABO08653 standard; protein; 440 AA.				
Best Local Similarity	26.0%;	Pred. No. 4.2e-10;	DE Human secreted/transmembrane protein (PRO) #17.				
RESULT 1442			PN US2003044923-A1.				
ID ABU84279 standard; protein; 440 AA.			PD 06-MAR-2003.				
DE Human secreted/transmembrane protein (PRO) #17.			Query Match	12.2%;	Score 220.5;	DB 6;	Length 440;
PN US2003032112-A1.			Best Local Similarity	26.0%;	Pred. No. 4.2e-10;		
PD 13-FEB-2003.			RESULT 1453				
Query Match	12.2%;	Score 220.5;	ID ABO02705 standard; protein; 440 AA.				
Best Local Similarity	26.0%;	Pred. No. 4.2e-10;	DE Human secreted/transmembrane protein (PRO) #17.				
RESULT 1443			PN US2003040062-A1.				
ID ABR66153 standard; protein; 440 AA.			PD 27-FEB-2003.				
DE Human secreted polypeptide PRO355, SEQ ID NO:34.			Query Match	12.2%;	Score 220.5;	DB 6;	Length 440;
PN US2003027278-A1.			Best Local Similarity	26.0%;	Pred. No. 4.2e-10;		
PD 06-FEB-2003.			RESULT 1454				
Query Match	12.2%;	Score 220.5;	ID ABR74859 standard; protein; 440 AA.				
Best Local Similarity	26.0%;	Pred. No. 4.2e-10;	DE Human secreted polypeptide PRO355, SEQ ID NO:34.				
RESULT 1444			PN US2003040056-A1.				
ID ABR65943 standard; protein; 440 AA.			PD 27-FEB-2003.				
DE Human secreted polypeptide PRO355, SEQ ID NO:34.			Query Match	12.2%;	Score 220.5;	DB 6;	Length 440;
PN US2003036159-A1.			Best Local Similarity	26.0%;	Pred. No. 4.2e-10;		
PD 20-FEB-2003.			RESULT 1455				
Query Match	12.2%;	Score 220.5;	ID ABR94621 standard; protein; 440 AA.				
Best Local Similarity	26.0%;	Pred. No. 4.2e-10;	DE Human secret				

RESULT 1457
ID ABU95594 standard; protein; 440 AA.
DE Human PRO polypeptide #17.
PN US2003036140-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 4.2e-10;
RESULT 1458
ID ABU98754 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO355.
PN US2003013153-A1.
PD 16-JAN-2003.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 4.2e-10;
RESULT 1459
ID ABU97969 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO355.
PN US2003017544-A1.
PD 23-JAN-2003.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 4.2e-10;
RESULT 1460
ID ABU91675 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO355.
PN US2003027277-A1.
PD 06-FEB-2003.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 4.2e-10;
RESULT 1461
ID ABU9368 standard; protein; 440 AA.
DE Human PRO polypeptide #17.
PN US2003036141-A1.
PD 20-FEB-2003.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 4.2e-10;
RESULT 1462
ID ABU96209 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #17.
PN US2003036146-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 4.2e-10;
RESULT 1463
ID ABU67422 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #17.
PN US2003036162-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 4.2e-10;
RESULT 1464
ID ABU80450 standard; protein; 440 AA.
DE Human PRO protein #17.
PN US2003036137-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 4.2e-10;
RESULT 1465
ID ABR99368 standard; protein; 440 AA.
DE Human secreted polypeptide PRO355, SEQ ID NO:34.
PN US2003040063-A1.
PD 27-FEB-2003.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 4.2e-10;
RESULT 1466
ID ABR98758 standard; protein; 440 AA.
DE Human secreted polypeptide PRO355, SEQ ID NO:34.
PN US2003040064-A1.
PD 27-FEB-2003.
Query Match 12.2%; Score 220.5; DB 6; Length 440;

Best Local Similarity 26.0%; Pred. No. 4.2e-10;
RESULT 1467
ID AB016281 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #17.
PN US2003027267-A1.
PD 06-FEB-2003.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 4.2e-10;
RESULT 1468
ID ABR92191 standard; protein; 440 AA.
DE Human secreted polypeptide PRO355, SEQ ID NO:34.
PN US2003036160-A1.
PD 20-FEB-2003.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 4.2e-10;
RESULT 1469
ID AB018822 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #17.
PN US2003044925-A1.
PD 06-MAR-2003.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 4.2e-10;
RESULT 1470
ID ABR78243 standard; protein; 440 AA.
DE Human secreted polypeptide PRO355, SEQ ID NO:34.
PN US2003054474-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 4.2e-10;
RESULT 1471
ID ABU64926 standard; protein; 440 AA.
DE Human secreted/transmembrane protein PRO355.
PN US2002173463-A1.
PD 21-NOV-2002.
PA (GETH) GENENTECH INC.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 4.2e-10;
RESULT 1472
ID ABU84979 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO355.
PN US2003032114-A1.
PD 13-FEB-2003.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 4.2e-10;
RESULT 1473
ID AB000118 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO355.
PN US2003032101-A1.
PD 13-FEB-2003.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 4.2e-10;
RESULT 1474
ID AB011450 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #17.
PN US2003036124-A1.
PD 20-FEB-2003.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 4.2e-10;
RESULT 1475
ID AB02095 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #17.
PN US2003040054-A1.
PD 27-FEB-2003.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 4.2e-10;
RESULT 1476
ID ABU58360 standard; protein; 440 AA.
DE Novel human secreted protein PRO355.
PN US2002150976-A1.
PD 17-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match 12.2%; Score 220.5; DB 6; Length 440;

Best Local Similarity 26.0%; Pred. No. 4.2e-10;
RESULT 1477
ID ABU8669 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO355.
PN US2003036133-A1.
PD 20-FEB-2003.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 4.2e-10;
RESULT 1478
ID ABU83364 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #17.
PN US2003036134-A1.
PD 20-FEB-2003.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 4.2e-10;
RESULT 1479
ID ABO06165 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO355.
PN US2003022294-A1.
PD 30-JAN-2003.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 4.2e-10;
RESULT 1480
ID ABR59201 standard; protein; 440 AA.
DE Human secreted polypeptide PRO355, SEQ ID NO:34.
PN US2003027275-A1.
PD 06-FEB-2003.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 4.2e-10;
RESULT 1481
ID ABO09263 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #17.
PN US2003027324-A1.
PD 06-FEB-2003.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 4.2e-10;
RESULT 1482
ID ABO19127 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO355.
PN US2003036118-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 4.2e-10;
RESULT 1483
ID ABO11145 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #17.
PN US2003036123-A1.
PD 20-FEB-2003.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 4.2e-10;
RESULT 1484
ID ABR66763 standard; protein; 440 AA.
DE Human secreted polypeptide PRO355, SEQ ID NO:34.
PN US2003036148-A1.
PD 20-FEB-2003.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 4.2e-10;
RESULT 1485
ID ABO15976 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #17.
PN US2003040060-A1.
PD 27-FEB-2003.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 4.2e-10;
RESULT 1486
ID ABO13682 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #17.
PN US2003044916-A1.
PD 06-MAR-2003.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 4.2e-10;
RESULT 1487
ID ABO07738 standard; protein; 440 AA.
DE Human PRO355 protein.
PN US2002142958-A1.
PD 03-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 4.2e-10;
RESULT 1488
ID ABU65585 standard; protein; 440 AA.
DE Human secreted/transmembrane protein, SEQ ID 34.
PN US2003036156-A1.
PD 20-FEB-2003.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 4.2e-10;
RESULT 1489
ID ABO07433 standard; protein; 440 AA.
DE Human PRO polypeptide #17.
PN US2003032117-A1.
PD 13-FEB-2003.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 4.2e-10;
RESULT 1490
ID ABO03620 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #17.
PN US2003036128-A1.
PD 20-FEB-2003.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 4.2e-10;
RESULT 1491
ID ABR67068 standard; protein; 440 AA.
DE Human secreted polypeptide PRO355, SEQ ID NO:34.
PN US2003027266-A1.
PD 06-FEB-2003.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 4.2e-10;
RESULT 1492
ID ABO15671 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #17.
PN US2003054483-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 4.2e-10;
RESULT 1493
ID ABUS5952 standard; protein; 440 AA.
DE Human secreted/transmembrane protein, PRO355.
PN US2003022298-A1.
PD 30-JAN-2003.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 4.2e-10;
RESULT 1494
ID ABU65280 standard; protein; 440 AA.
DE Human PRO polypeptide #17.
PN US2003032102-A1.
PD 13-FEB-2003.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 4.2e-10;
RESULT 1495
ID ABU95225 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO355.
PN US2003036117-A1.
PD 20-FEB-2003.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 4.2e-10;
RESULT 1496
ID ABU71128 standard; protein; 440 AA.
DE Human PRO355 protein.
PN US2003036143-A1.
PD 20-FEB-2003.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 4.2e-10;
RESULT 1497
ID ABO07738 standard; protein; 440 AA.

DE Human PRO polypeptide #17.
PN US2003012130-A1.
PD 13-FEB-2003.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 4.2e-10;
RESULT 1498
ID ABR69979 standard; protein; 440 AA.
DE Human secreted polypeptide PRO355, SEQ ID NO:34.
PN US2003012138-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 4.2e-10;
RESULT 1499
ID ABR69312 standard; protein; 440 AA.
DE Human secreted polypeptide PRO355, SEQ ID NO:34.
PN US2003036132-A1.
PD 20-FEB-2003.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 4.2e-10;
RESULT 1500
ID ABO01453 standard; protein; 440 AA.
DE Human PRO polypeptide #17.
PN US2003008353-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 4.2e-10;

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OM protein - protein search, using sw model

Run on: October 21, 2006, 18:05:31 ; Search time 52 Seconds
 (without alignments)
 579.049 Million cell updates/sec

Perfect score: 1806
 Sequence: 1 MKTIQPKMHNSISWAIFTGL.....RRAGCVWLLPLVLHLLKF 344

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 1500 summaries

Database : Issued Patents AA:*

- 1: /EMC_Celerra_SIDS3/ptodata/2/iaa/5_COMB.pep:*
- 2: /EMC_Celerra_SIDS3/ptodata/2/iaa/6_COMB.pep:*
- 3: /EMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB.pep:*
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- 5: /EMC_Celerra_SIDS3/ptodata/2/iaa/PCFUS_COMB.pep:*
- 6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*
- 7: /EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution:

Result		Query		Description	
No.	Score	Match	Length	ID	
1	1806	100.0	344	2	US-09-700-397-3 Sequence 3, Appli
9	1642	90.9	313	2	US-09-700-397-4 Sequence 4, Appli
10	931.5	51.6	338	2	US-09-976-594-404 Sequence 404, Appl
11	926.5	51.3	338	1	US-08-414-657D-42 Sequence 42, Appl
12	926.5	51.3	338	1	US-08-414-657D-43 Sequence 43, Appl
13	926.5	51.3	338	2	US-09-135-080-4 Sequence 4, Appli
14	923.5	51.1	325	1	US-08-414-657D-2 Sequence 2, Appli
15	923.5	51.1	325	1	US-08-414-657D-41 Sequence 41, Appli
16	923.5	51.1	325	2	US-09-135-080-2 Sequence 2, Appli
17	923.5	51.1	338	1	US-08-414-657D-60 Sequence 60, Appl
18	923.5	51.1	338	2	US-09-135-080-8 Sequence 8, Appli
19	908	50.3	308	1	US-08-414-657D-46 Sequence 46, Appl
20	907	50.2	315	1	US-08-414-657D-47 Sequence 47, Appl
21	905	50.1	310	1	US-08-414-657D-45 Sequence 45, Appl
22	902	49.9	304	1	US-08-414-657D-44 Sequence 44, Appl
23	886.5	48.1	287	1	US-08-414-657D-48 Sequence 48, Appl
24	885.5	49.0	287	1	US-08-414-657D-49 Sequence 49, Appl
25	820	45.4	354	2	US-10-104-047-2365 Sequence 2365, Ap
33	796.5	44.1	252	1	US-08-414-657D-56 Sequence 56, Appl
34	795.5	44.0	252	1	US-08-414-657D-57 Sequence 57, Appl
35	742.5	41.1	212	2	US-09-949-016-10458 Sequence 10458, A
36	288.5	16.0	961	3	US-10-162-335-42 Sequence 42, Appl
37	288.5	16.0	4126	2	US-09-953-096-4 Sequence 4, Appli
38	288.5	16.0	5518	2	US-09-953-096-2 Sequence 2, Appli
39	276	15.3	588	2	US-09-949-016-10547 Sequence 10547, A
40	276	15.3	733	2	US-10-094-749-3192 Sequence 3192, Ap
41	276	15.3	848	2	US-09-787-443-44 Sequence 44, Appli

SUMMARIES

14.8	267	58	2	US-09-513-999C-6852	Sequence 6852, Ap
14.5	261	1395	2	US-09-540-245A-15	Sequence 15, Appl
14.5	261	1395	2	US-10-289-776-15	Sequence 15, Appl
14.5	261	1395	3	US-09-191-651-2	Sequence 2, Appli
14.2	256	421	1	US-08-659-984A-1	Sequence 1, Appli
14.2	256	421	2	US-08-660-531-1	Sequence 1, Appli
14.2	256	421	2	US-09-404-578-1	Sequence 1, Appli
14.2	256	444	1	US-08-659-984A-5	Sequence 5, Appli
14.2	256	444	2	US-08-660-531-5	Sequence 5, Appli
14.2	256	444	2	US-09-404-578-5	Sequence 5, Appli
13.8	249.5	607	1	US-08-752-307B-12	Sequence 12, Appl
13.8	249.5	607	2	US-09-707-802-12	Sequence 12, Appl
13.8	249.5	607	2	US-09-991-326-12	Sequence 12, Appl
13.6	246.5	1007	3	US-10-329-258-23	Sequence 23, Appl
13.6	246.5	1018	1	US-08-408-093-6	Sequence 6, Appli
13.6	246.5	1018	1	US-08-408-420A-6	Sequence 6, Appli
13.6	246.5	1018	1	US-08-714-901-6	Sequence 6, Appli
13.6	246.5	1018	2	US-08-040-741-6	Sequence 6, Appli
13.6	246.5	1044	2	US-09-949-016-10321	Sequence 10321, A
13.5	244.5	512	2	US-10-094-749-2493	Sequence 2493, Ap
13.5	243.5	605	2	US-08-752-307B-8	Sequence 8, Appli
13.5	243.5	605	2	US-09-707-802-8	Sequence 8, Appli
13.5	243.5	605	2	US-09-991-326-8	Sequence 8, Appli
13.5	243.5	1018	1	US-08-452-052-2	Sequence 2, Appli
13.4	241.5	837	2	US-09-949-016-6515	Sequence 6515, Ap
13.2	237.5	819	2	US-09-949-016-11044	Sequence 11044, A
13.1	237	73	1	US-08-414-657D-50	Sequence 50, Appl
13.1	237	73	1	US-08-414-657D-51	Sequence 51, Appl
12.8	230.5	868	1	US-08-374-834-1	Sequence 1, Appli
12.8	230.5	868	1	US-08-644-271-1	Sequence 1, Appli
12.8	230.5	868	2	US-09-077-955-1	Sequence 1, Appli
12.8	230.5	868	2	US-10-016-283-1	Sequence 1, Appli
12.7	229.5	869	1	US-08-374-834-16	Sequence 16, Appl
12.7	229.5	869	2	US-08-644-271-29	Sequence 29, Appl
12.7	229.5	869	2	US-09-077-955-33	Sequence 33, Appl
12.7	229.5	869	2	US-10-016-283-33	Sequence 33, Appl
12.5	225.5	478	5	PCT-US95-08493-15	Sequence 15, Appl
12.5	225.5	860	5	PCT-US95-08493-19	Sequence 19, Appl
12.5	225.5	868	5	PCT-US95-08493-21	Sequence 21, Appl
12.5	225.5	4391	2	US-10-006-011A-2	Sequence 2, Appli
12.4	224.5	869	2	US-09-715-249-8	Sequence 8, Appli
12.3	222.5	504	2	US-09-270-767-43244	Sequence 2641, Ap
12.3	222.5	504	2	US-09-270-767-43244	Sequence 43244, A
12.2	221	1571	2	US-08-956-991-11	Sequence 11, Appl
12.2	221	1910	2	US-08-956-991-2	Sequence 2, Appli
12.2	220.5	423	2	US-08-778-510-22	Sequence 22, Appl
12.2	220.5	442	2	US-09-944-457-61	Sequence 61, Appl
12.2	220.5	442	2	US-09-778-510-20	Sequence 20, Appl
12.2	220.5	442	2	US-09-930-803-1	Sequence 1, Appli
12.1	219	1091	2	US-08-986-485-5	Sequence 5, Appli
12.1	219	1101	2	US-08-986-485-2	Sequence 2, Appli
11.8	213.5	398	2	US-09-778-510-6	Sequence 6, Appli
11.8	213	59	1	US-08-414-657D-52	Sequence 52, Appl
11.7	212	59	1	US-08-414-657D-53	Sequence 53, Appl
11.7	211.5	1070	2	US-09-961-403-3	Sequence 3, Appli
11.7	211.5	1461	2	US-09-976-594-531	Sequence 531, App
11.7	211.5	398	2	US-08-778-510-4	Sequence 4, Appli
11.7	211	615	2	US-08-752-307B-9	Sequence 9, Appli
11.7	211	615	1	US-09-707-802-9	Sequence 9, Appli
11.7	211	615	2	US-09-991-326-9	Sequence 9, Appli
11.7	211	7968	3	US-10-077-130-5	Sequence 5, Appli
11.6	210	191	2	US-09-270-767-32640	Sequence 32640, A
11.6	210	1953	2	US-09-917-254-92	Sequence 92, Appl
11.6	209	504	2	US-09-949-016-7020	Sequence 7020, Ap
11.6	209	511	2	US-09-949-016-10054	Sequence 10054, A
11.5	208.5	1651	2	US-09-540-245A-18	Sequence 18, Appl
11.5	208.5	1651	2	US-10-289-776-18	Sequence 18, Appl
11.5	208.5	1651	3	US-09-191-651-8	Sequence 8, Appli
11.5	207.5	329	2	US-10-104-047-3709	Sequence 3709, Ap
11.5	207.5	596	1	US-08-752-307B-13	Sequence 13, Appl
11.4	205.5	596	2	US-09-707-802-13	Sequence 13, Appl
11.4	205.5	596	2	US-09-991-326-13	Sequence 13, Appl
11.4	205	432	2	US-09-778-510-2	Sequence 2, Appli

201	201	11.1	946	5	PCT-US95-08493-13	Sequence 13, Appl	281	171.5	9.5	780	1	US-08-786-164-14	Sequence 14, Appl
202	199	11.0	1241	2	US-09-040-774-2	Sequence 2, Appl	282	171.5	9.5	1338	2	US-08-750-141A-3	Sequence 3, Appl
203	198	11.0	847	2	US-09-949-002-328	Sequence 328, App	283	171.5	9.5	1338	2	US-09-119-014D-6	Sequence 6, Appl
204	198	11.0	862	2	US-09-949-002-427	Sequence 427, App	284	171.5	9.5	464	1	US-08-602-725-32	Sequence 32, Appl
205	198	11.0	1709	2	US-09-949-016-10503	Sequence 10503, A	285	171.5	9.5	464	2	US-09-949-016-6116	Sequence 6116, Ap
206	197.5	10.9	1447	2	US-09-041-886-12053	Sequence 25, Appl	286	171.5	9.5	464	2	US-09-949-016-7525	Sequence 7525, Ap
207	197.5	10.9	1447	5	PCT-US94-05277-2	Sequence 2, Appl	287	171.5	9.5	917	1	US-08-245-295-2	Sequence 2, Appl
208	197	10.9	1297	2	US-09-540-245A-17	Sequence 17, Appl	288	171.5	9.5	917	1	US-08-481-130-2	Sequence 2, Appl
209	197	10.9	1297	2	US-10-289-776-17	Sequence 17, Appl	289	171.5	9.5	917	1	US-08-656-984A-2	Sequence 2, Appl
210	197	10.9	1297	3	US-09-191-651-6	Sequence 6, Appl	290	171.5	9.5	917	1	US-08-485-604-2	Sequence 2, Appl
211	196.5	10.9	686	3	US-10-162-335-48	Sequence 48, Appl	291	171.5	9.5	917	1	US-08-487-595-2	Sequence 2, Appl
212	196.5	10.9	686	3	US-10-162-335-52	Sequence 52, Appl	292	171.5	9.5	1253	1	US-08-506-296B-14	Sequence 14, Appl
213	196.5	10.9	833	2	US-09-949-016-11496	Sequence 11496, A	293	170.5	9.4	318	2	US-09-068-051A-32	Sequence 32, Appl
214	186.5	10.9	1180	2	US-09-949-016-6577	Sequence 6577, Ap	294	167.5	9.3	280	2	US-09-270-767-43068	Sequence 43068, A
215	195.5	10.8	686	3	US-10-162-335-46	Sequence 46, Appl	295	167.5	9.3	466	1	US-08-432-016-4	Sequence 4, Appl
216	195.5	10.8	686	3	US-10-162-335-46	Sequence 46, Appl	296	167.5	9.3	466	1	US-08-684-594-4	Sequence 4, Appl
217	195	10.8	630	1	US-08-752-307B-14	Sequence 14, Appl	297	167.5	9.2	668	1	US-08-232-538-13	Sequence 13, Appl
218	195	10.8	630	2	US-09-707-802-14	Sequence 14, Appl	298	167.5	9.2	668	1	US-08-786-164-13	Sequence 14, Appl
219	195	10.8	630	2	US-09-991-326-14	Sequence 14, Appl	299	167.5	9.2	764	2	US-09-142-956B-14	Sequence 2, Appl
220	195	10.8	1034	2	US-10-094-749-2631	Sequence 2631, Ap	300	167.5	9.2	767	1	US-08-874-678-2	Sequence 2, Appl
221	194.5	10.8	686	3	US-10-162-335-50	Sequence 50, Appl	301	167.5	9.2	767	2	US-08-643-839-2	Sequence 2, Appl
222	192.5	10.7	612	1	US-08-752-307B-11	Sequence 11, Appl	302	167.5	9.2	767	2	US-09-348-886-2	Sequence 2, Appl
223	192.5	10.7	612	2	US-09-707-802-11	Sequence 11, Appl	303	167.5	9.2	767	2	US-10-105-901A-2	Sequence 2, Appl
224	192.5	10.7	612	2	US-09-991-326-11	Sequence 11, Appl	304	167.5	9.2	788	1	US-08-232-538-15	Sequence 15, Appl
225	192.5	10.7	826	2	US-09-877-730-16	Sequence 16, Appl	305	167.5	9.2	788	1	US-08-786-164-15	Sequence 15, Appl
226	192.5	10.7	904	2	US-09-877-730-6	Sequence 6, Appl	306	167.5	9.2	1356	1	US-08-810-116-8	Sequence 8, Appl
227	192.5	10.7	907	2	US-09-877-730-20	Sequence 20, Appl	307	167.5	9.2	1356	1	US-07-930-548A-8	Sequence 8, Appl
228	192.5	10.7	983	2	US-09-412-554A-2	Sequence 2, Appl	308	167.5	9.2	1356	2	US-09-098-707A-2	Sequence 2, Appl
229	192.5	10.7	985	2	US-09-877-730-10	Sequence 10, Appl	309	167.5	9.2	1356	2	US-09-483-539-2	Sequence 2, Appl
230	192.5	10.7	985	2	US-09-877-730-12	Sequence 12, Appl	310	167.5	9.2	1356	2	US-09-949-016-6198	Sequence 6198, Ap
231	192.5	10.7	1069	2	US-09-877-730-2	Sequence 2, Appl	311	167.5	9.2	1356	2	US-10-100-405A-2	Sequence 2, Appl
232	192.5	10.7	1072	2	US-09-877-730-18	Sequence 18, Appl	312	167.5	9.2	1356	2	US-10-022-939-2	Sequence 2, Appl
233	192.5	10.7	1150	2	US-09-877-730-8	Sequence 8, Appl	313	167.5	9.2	1456	2	US-09-949-016-9853	Sequence 9853, Ap
234	192.5	10.7	1260	2	US-08-506-296B-21	Sequence 21, Appl	314	166.5	9.2	302	2	US-09-877-730-14	Sequence 14, Appl
235	192.5	10.7	1268	2	US-08-506-296B-28	Sequence 28, Appl	315	166.5	9.2	380	2	US-09-877-730-4	Sequence 4, Appl
236	192	10.6	529	2	US-09-383-586-31	Sequence 31, Appl	316	166.5	9.2	758	2	US-08-874-678-1	Sequence 1, Appl
237	192	10.6	529	2	US-09-823-038A-31	Sequence 31, Appl	317	166.5	9.2	758	2	US-08-643-839-1	Sequence 1, Appl
238	192	10.6	650	2	US-10-104-047-3395	Sequence 3395, Ap	318	166.5	9.2	758	2	US-09-051-363-24	Sequence 24, Appl
239	191.5	10.6	1209	2	US-09-130-158A-2	Sequence 2, Appl	319	166.5	9.2	758	2	US-09-348-886-1	Sequence 1, Appl
240	188.5	10.4	651	2	US-09-270-767-44877	Sequence 44877, A	320	166.5	9.2	758	2	US-10-105-901A-1	Sequence 1, Appl
241	187.5	10.4	1266	1	US-08-506-296B-4	Sequence 4, Appl	321	166.5	9.2	758	2	US-09-499-468-39	Sequence 39, Appl
242	185.5	10.3	318	1	US-08-633-148-4	Sequence 4, Appl	322	165.5	9.2	278	1	US-08-432-016-5	Sequence 5, Appl
243	185.5	10.3	332	2	US-09-082-365-1	Sequence 1, Appl	323	165.5	9.2	278	1	US-08-684-594-5	Sequence 5, Appl
244	185.5	10.3	339	2	US-09-799-152-2	Sequence 2, Appl	324	165.5	9.2	486	1	US-08-432-016-6	Sequence 6, Appl
245	185.5	10.3	340	1	US-08-633-148-2	Sequence 2, Appl	325	165.5	9.2	486	1	US-08-684-594-6	Sequence 6, Appl
246	185.5	10.3	404	2	US-09-949-016-11025	Sequence 11025, A	326	165.5	9.2	583	1	US-08-432-016-2	Sequence 2, Appl
247	185.5	10.3	404	2	US-09-799-152-1	Sequence 1, Appl	327	165.5	9.2	583	1	US-08-684-594-2	Sequence 2, Appl
248	185.5	10.3	642	1	US-08-217-299-1	Sequence 1, Appl	328	165.5	9.2	646	2	US-09-949-016-6728	Sequence 6728, Ap
249	185.5	10.3	698	1	US-08-602-725-36	Sequence 36, Appl	329	165.5	9.2	646	2	US-09-653-961-4	Sequence 4, Appl
250	185.5	10.3	702	2	US-09-949-016-6484	Sequence 6484, Ap	330	165.5	9.2	828	1	US-08-261-304-2	Sequence 2, Appl
251	185.5	10.3	734	1	US-08-389-459A-17	Sequence 17, Appl	331	165.5	9.2	1617	2	US-09-784-358-16	Sequence 16, Appl
252	185.5	10.3	734	2	US-08-987-867A-17	Sequence 17, Appl	332	165.5	9.2	1691	2	US-09-784-358-2	Sequence 2, Appl
253	185.5	10.3	740	2	US-09-949-016-8168	Sequence 8168, Ap	333	165.5	9.1	501	1	US-08-408-095-31	Sequence 31, Appl
254	185	10.2	1381	2	US-09-540-245A-16	Sequence 16, Appl	334	164.5	9.1	1194	2	US-10-191-029-10	Sequence 10, Appl
255	185	10.2	1381	2	US-10-289-776-16	Sequence 16, Appl	335	164.5	9.1	439	2	US-09-383-586-32	Sequence 32, Appl
256	185	10.2	1381	3	US-09-191-651-4	Sequence 4, Appl	336	164.5	9.1	439	2	US-09-823-038A-32	Sequence 32, Appl
257	185	10.2	2596	2	US-09-548-473B-6	Sequence 6, Appl	337	164.5	9.1	640	2	US-09-949-016-7565	Sequence 7565, Ap
258	185	10.2	2630	3	US-10-077-130-2	Sequence 2, Appl	338	163.5	9.1	582	2	US-09-702-705-334	Sequence 334, App
259	184.5	10.2	66	1	US-08-414-657D-54	Sequence 54, Appl	339	163.5	9.1	582	2	US-09-736-457-334	Sequence 334, App
260	184.5	10.2	66	1	US-08-414-657D-55	Sequence 55, Appl	340	163.5	9.1	582	2	US-09-614-124B-334	Sequence 334, App
261	184.5	10.2	404	2	US-09-638-649-3	Sequence 3, Appl	341	163.5	9.1	582	2	US-09-671-325-334	Sequence 334, App
262	184.5	10.2	404	2	US-09-638-648-3	Sequence 3, Appl	342	163.5	9.1	582	2	US-09-589-184-334	Sequence 334, App
263	184	10.2	373	2	US-09-823-038A-60	Sequence 60, Appl	343	163.5	9.1	582	2	US-09-658-824-334	Sequence 334, App
264	184	10.2	405	2	US-08-755-235-4	Sequence 4, Appl	344	163.5	9.1	582	2	US-10-017-754-334	Sequence 334, App
265	182	10.1	626	2	US-09-949-016-6213	Sequence 6213, Ap	345	163.5	9.1	582	2	US-09-651-563-334	Sequence 334, App
266	182	10.1	664	2	US-09-949-016-7850	Sequence 7850, Ap	346	163.5	9.1	582	2	US-09-519-642-334	Sequence 334, App
267	181	10.0	885	2	US-10-104-047-2946	Sequence 2946, Ap	347	163.5	9.1	604	2	US-09-949-016-9548	Sequence 9548, Ap
268	179	9.9	300	2	US-09-254-465A-10	Sequence 10, Appl	348	163.5	9.1	623	2	US-09-949-016-11206	Sequence 11206, A
269	179	9.9	300	2	US-09-397-243D-12	Sequence 12, Appl	349	163.5	9.1	646	2	US-09-653-961-2	Sequence 2, Appl
270	179	9.9	300	2	US-09-953-499-10	Sequence 10, Appl	350	163.5	9.1	1745	2	US-09-800-729-89	Sequence 89, Appl
271	174	9.6	261	2	US-09-270-767-32898	Sequence 32898, A	351	163.5	9.0	924	1	US-08-481-130-28	Sequence 28, Appl
272	174	9.6	261	2	US-09-270-767-48115	Sequence 48115, A	352	163.5	9.0	924	1	US-08-656-984A-28	Sequence 28, Appl
280	171.5	9.5	780	1	US-08-232-538-14	Sequence 14, Appl	353	163.5	9.0	924	1	US-08-485-604-28	Sequence 28, Appl

354	163	9.0	924	1	US-08-487-595-28	Sequence 28, Appl	481	155	8.6	1248	2	US-09-949-016-10596	Sequence 10596, A
355	162	9.0	321	7	5169835-17	Patent No. 5169835	482	155	8.6	1363	2	US-09-375-248-19	Sequence 19, Appl
356	161	8.9	622	1	US-09-499-846-2	Sequence 2, Appl	483	155	8.6	1367	1	US-07-813-593-4	Sequence 4, Appl
376	161	8.9	806	1	US-08-443-861-5	Sequence 5, Appl	484	155	8.6	1367	1	US-07-977-451-6	Sequence 6, Appl
377	161	8.9	806	2	US-08-193-8298-5	Sequence 5, Appl	485	155	8.6	1367	1	US-07-946-507-4	Sequence 4, Appl
378	161	8.9	806	2	US-09-766-678-5	Sequence 5, Appl	486	155	8.6	1367	1	US-08-252-517-6	Sequence 6, Appl
379	161	8.9	816	1	US-07-640-023-1	Sequence 1, Appl	487	155	8.6	1367	1	US-07-906-397A-6	Sequence 6, Appl
380	161	8.9	820	1	US-07-921-807B-3	Sequence 3, Appl	488	155	8.6	1367	1	US-08-601-891-6	Sequence 6, Appl
381	161	8.9	820	1	US-08-441-944A-3	Sequence 3, Appl	489	155	8.6	1367	1	US-09-021-324-6	Sequence 6, Appl
382	161	8.9	820	2	US-08-439-992A-1	Sequence 1, Appl	490	155	8.6	1367	2	US-09-872-136B-6	Sequence 6, Appl
383	161	8.9	820	2	US-09-620-561-1	Sequence 1, Appl	491	155	8.6	1367	2	US-09-919-408A-6	Sequence 6, Appl
384	161	8.9	1367	1	US-08-443-861-2	Sequence 2, Appl	492	155	8.6	1367	5	PCT-US92-02750-8	Sequence 8, Appl
385	161	8.9	1367	2	US-08-193-8298-2	Sequence 2, Appl	493	155	8.6	1367	5	PCT-US92-05401-6	Sequence 6, Appl
386	161	8.9	1367	2	US-09-766-678-2	Sequence 2, Appl	494	155	8.6	1367	5	PCT-US92-09893-6	Sequence 6, Appl
387	160.5	8.9	316	2	US-09-397-243D-13	Sequence 13, Appl	495	154.5	8.6	306	2	US-10-191-029-12	Sequence 12, Appl
388	160	8.9	270	2	US-09-254-465A-24	Sequence 24, Appl	496	154.5	8.6	462	1	US-08-752-307B-7	Sequence 7, Appl
389	160	8.9	270	2	US-09-953-499-24	Sequence 24, Appl	497	154.5	8.6	462	2	US-09-707-802-7	Sequence 7, Appl
390	160	8.9	273	2	US-09-254-465A-26	Sequence 26, Appl	498	154.5	8.6	462	2	US-09-991-326-7	Sequence 7, Appl
391	160	8.9	273	2	US-09-953-499-26	Sequence 26, Appl	499	154.5	8.6	465	1	US-08-752-307B-5	Sequence 5, Appl
392	160	8.9	319	1	US-08-597-495B-22	Sequence 22, Appl	500	154.5	8.6	465	2	US-09-707-802-5	Sequence 5, Appl
393	160	8.9	319	2	US-09-068-051A-22	Sequence 22, Appl	501	154.5	8.6	465	2	US-09-991-326-5	Sequence 5, Appl
394	160	8.9	319	2	US-09-336-536-67	Sequence 67, Appl	502	154.5	8.6	602	1	US-08-428-926-5	Sequence 5, Appl
395	160	8.9	319	2	US-09-254-465A-6	Sequence 6, Appl	503	154.5	8.6	602	1	US-08-428-926-5	Sequence 5, Appl
396	160	8.9	319	2	US-09-953-499-6	Sequence 6, Appl	504	154.5	8.6	602	1	US-08-428-298-5	Sequence 5, Appl
397	160	8.9	609	2	US-09-949-016-7747	Sequence 7747, Ap	505	154.5	8.6	602	1	US-08-339-517-5	Sequence 5, Appl
398	160	8.9	609	2	US-09-949-016-7748	Sequence 7748, Ap	506	154.5	8.6	1311	1	US-08-340-011-5	Sequence 5, Appl
399	160	8.9	609	2	US-09-949-016-7749	Sequence 7749, Ap	507	154.5	8.6	1311	2	US-08-901-710-5	Sequence 5, Appl
400	160	8.9	609	2	US-09-949-016-7750	Sequence 7750, Ap	508	154.5	8.6	1311	2	US-09-169-079-5	Sequence 5, Appl
401	160	8.9	609	2	US-09-949-016-7751	Sequence 7751, Ap	509	154.5	8.6	1311	3	US-09-765-534B-5	Sequence 5, Appl
402	160	8.9	609	2	US-09-949-016-7752	Sequence 7752, Ap	510	154	8.5	579	2	US-09-173-151A-2	Sequence 2, Appl
403	160	8.9	609	2	US-09-949-016-7753	Sequence 7753, Ap	511	154	8.5	686	2	US-09-173-151A-4	Sequence 4, Appl
404	160	8.9	609	2	US-09-949-016-7754	Sequence 7754, Ap	512	153.5	8.5	477	1	US-08-432-016-3	Sequence 3, Appl
405	160	8.9	817	1	US-07-640-023-2	Sequence 2, Appl	513	153.5	8.5	477	1	US-08-684-594-3	Sequence 3, Appl
406	160	8.9	822	1	US-07-921-807B-4	Sequence 4, Appl	514	153	8.5	189	2	US-08-270-767-32726	Sequence 32726, A
407	160	8.9	822	1	US-08-459-296-2	Sequence 2, Appl	515	153	8.5	189	2	US-09-270-767-47943	Sequence 47943, A
408	160	8.9	822	1	US-08-441-944A-4	Sequence 4, Appl	516	153	8.5	524	2	US-09-270-767-44009	Sequence 44009, A
409	160	8.9	822	1	US-08-451-822A-12	Sequence 12, Appl	517	153	8.5	894	2	US-09-949-016-10605	Sequence 10605, A
410	160	8.9	822	2	US-08-439-992A-2	Sequence 2, Appl	518	152	8.4	351	5	PCT-US93-05703-2	Sequence 2, Appl
411	160	8.9	822	2	US-08-323-430-12	Sequence 12, Appl	519	152	8.4	1123	2	US-09-949-016-6230	Sequence 6230, Ap
412	160	8.9	822	2	US-09-620-561-2	Sequence 2, Appl	520	152	8.4	1128	2	US-09-949-016-7522	Sequence 7522, Ap
413	158.5	8.8	822	1	US-09-677-046A-4	Sequence 1, Appl	521	151.5	8.4	422	2	US-09-205-258-947	Sequence 947, App
414	158.5	8.8	1474	2	US-09-677-046A-2	Sequence 4, Appl	522	151.5	8.4	422	2	US-10-004-860-947	Sequence 947, App
415	158.5	8.8	1509	2	US-09-800-729-175	Sequence 2, Appl	523	151.5	8.4	365	2	US-09-949-016-7591	Sequence 7591, Ap
416	158	8.7	292	2	US-09-800-729-175	Sequence 175, App	524	151.5	8.4	422	1	US-08-036-555B-170	Sequence 170, App
417	158	8.7	611	1	US-08-752-307B-10	Sequence 10, Appl	525	151.5	8.4	422	1	US-08-469-569-170	Sequence 170, App
418	158	8.7	611	2	US-09-707-802-10	Sequence 10, Appl	526	151.5	8.4	422	1	US-08-428-926-3	Sequence 3, Appl
419	158	8.7	611	2	US-09-991-326-10	Sequence 10, Appl	527	151.5	8.4	422	1	US-08-249-322A-170	Sequence 170, App
420	158	8.7	736	5	PCT-US93-00031-15	Sequence 15, Appl	528	151.5	8.4	422	1	US-08-428-927-3	Sequence 3, Appl
421	157.5	8.7	1503	2	US-09-677-046A-6	Sequence 6, Appl	529	151.5	8.4	422	1	US-08-428-298-3	Sequence 3, Appl
422	157	8.7	260	2	US-09-254-465A-23	Sequence 23, Appl	530	151.5	8.4	422	1	US-08-339-517-3	Sequence 3, Appl
423	157	8.7	260	2	US-09-953-499-23	Sequence 23, Appl	531	151.5	8.4	422	1	US-08-469-526A-170	Sequence 170, App
424	157	8.7	263	2	US-09-254-465A-25	Sequence 25, Appl	532	151.5	8.4	422	1	US-08-734-531A-170	Sequence 170, App
425	157	8.7	263	2	US-09-953-499-25	Sequence 25, Appl	533	151.5	8.4	422	1	US-08-469-660-170	Sequence 170, App
426	157	8.7	299	2	US-09-188-930-331	Sequence 331, App	534	151.5	8.4	422	2	US-08-341-018-72	Sequence 72, Appl
427	157	8.7	299	2	US-09-462-270-2	Sequence 2, Appl	535	151.5	8.4	422	2	US-08-470-335-170	Sequence 170, App
428	157	8.7	299	2	US-09-254-465A-1	Sequence 1, Appl	536	151.5	8.4	422	2	US-08-735-021-170	Sequence 170, App
429	157	8.7	299	2	US-09-312-283C-189	Sequence 189, App	537	151.5	8.4	422	2	US-08-734-664A-170	Sequence 170, App
430	157	8.7	299	2	US-09-312-283C-331	Sequence 331, App	538	151.5	8.4	422	2	US-08-470-339-170	Sequence 170, App
431	157	8.7	299	2	US-09-312-283C-331	Sequence 331, App	539	151.5	8.4	422	2	US-08-467-602-170	Sequence 170, App
432	157	8.7	299	2	US-09-953-499-1	Sequence 1, Appl	540	151.5	8.4	422	2	US-08-411-295F-65	Sequence 65, Appl
433	156.5	8.7	416	2	US-09-638-649-1	Sequence 1, Appl	541	151.5	8.4	422	2	US-08-411-295F-66	Sequence 66, Appl
434	156.5	8.7	416	2	US-08-755-235-2	Sequence 2, Appl	542	151.5	8.4	422	2	US-08-411-295F-69	Sequence 69, Appl
435	156.5	8.7	416	2	US-09-638-648-1	Sequence 1, Appl	543	151.5	8.4	422	2	US-08-411-295F-103	Sequence 103, App
436	155.5	8.6	880	1	US-08-445-640-10	Sequence 10, Appl	544	151.5	8.4	422	5	PCT-US94-05083C-166	Sequence 166, App
437	155.5	8.6	880	1	US-08-445-640-10	Sequence 10, Appl	545	151.5	8.4	422	5	PCT-US94-05083C-185	Sequence 185, App
438	155.5	8.6	880	2	US-08-170-558-10	Sequence 10, Appl	546	151.5	8.4	422	5	PCT-US95-06846A-170	Sequence 170, App
439	155.5	8.6	880	2	US-08-447-314-10	Sequence 10, Appl	547	151.5	8.4	1363	1	US-08-874-678-32	Sequence 32, Appl
440	155.5	8.6	880	2	US-08-445-461-10	Sequence 10, Appl	548	151.5	8.4	1363	2	US-08-643-839-32	Sequence 32, Appl
441	155.5	8.6	880	2	US-09-223-490-10	Sequence 10, Appl	549	151.5	8.4	1363	2	US-09-348-886-32	Sequence 32, Appl
442	155.5	8.6	880	3	US-10-646-760-10	Sequence 10, Appl	550	151.5	8.4	1363	2	US-10-105-901A-32	Sequence 32, Appl
443	155	8.6	805	2	US-08-985-526-34	Sequence 34, Appl	551	151	8.4	874	1	US-08-456-647B-6	Sequence 6, Appl
444	155	8.6	1248	2	US-09-949-016-10595	Sequence 10595, A	552	151	8.4	874	1	US-08-237-401A-6	Sequence 6, Appl
445	155	8.6					553	150.5	8.3	349	2	US-09-924-103-4	Sequence 4, Appl

554	150.5	8.3	411	2	US-08-470-339-189	Sequence 189, App	627	150.5	8.3	865	2	US-08-411-295F-248	Sequence 248, App
555	150.5	8.3	414	2	US-08-470-339-188	Sequence 188, App	628	150.5	8.3	868	2	US-08-470-335-229	Sequence 229, App
556	150.5	8.3	422	2	US-08-467-602-324	Sequence 324, App	629	150.5	8.3	868	2	US-08-467-602-317	Sequence 317, App
557	150.5	8.3	422	2	US-08-411-295F-250	Sequence 250, App	630	150.5	8.3	868	2	US-08-411-295F-243	Sequence 243, App
558	150.5	8.3	425	2	US-08-470-335-226	Sequence 320, App	631	150.5	8.3	874	2	US-08-470-335-238	Sequence 238, App
559	150.5	8.3	425	2	US-08-467-602-320	Sequence 320, App	632	150.5	8.3	874	2	US-08-467-602-334	Sequence 334, App
560	150.5	8.3	425	2	US-08-411-295F-246	Sequence 246, App	633	150.5	8.3	874	2	US-08-411-295F-260	Sequence 260, App
561	150.5	8.3	445	2	US-08-467-602-328	Sequence 328, App	634	150.5	8.3	875	2	US-08-467-602-369	Sequence 369, App
562	150.5	8.3	445	2	US-08-411-295F-254	Sequence 254, App	635	150.5	8.3	875	2	US-08-411-295F-295	Sequence 295, App
563	150.5	8.3	456	2	US-08-467-602-366	Sequence 366, App	636	150.5	8.3	877	2	US-08-470-335-232	Sequence 232, App
564	150.5	8.3	456	2	US-08-411-295F-292	Sequence 292, App	637	150.5	8.3	877	2	US-08-467-602-331	Sequence 331, App
565	150.5	8.3	459	2	US-08-467-602-362	Sequence 362, App	638	150.5	8.3	877	2	US-08-411-295F-257	Sequence 257, App
566	150.5	8.3	459	2	US-08-411-295F-288	Sequence 288, App	639	150.5	8.3	884	2	US-08-467-602-378	Sequence 378, App
567	150.5	8.3	479	2	US-08-467-602-370	Sequence 370, App	640	150.5	8.3	884	2	US-08-411-295F-304	Sequence 304, App
568	150.5	8.3	601	2	US-08-411-295F-296	Sequence 296, App	641	150.5	8.3	888	2	US-08-467-602-325	Sequence 325, App
569	150.5	8.3	601	2	US-08-470-335-233	Sequence 233, App	642	150.5	8.3	888	2	US-08-411-295F-251	Sequence 251, App
570	150.5	8.3	601	2	US-08-467-602-323	Sequence 323, App	643	150.5	8.3	897	2	US-08-467-602-337	Sequence 337, App
571	150.5	8.3	601	2	US-08-411-295F-249	Sequence 249, App	644	150.5	8.3	897	2	US-08-411-295F-263	Sequence 263, App
572	150.5	8.3	604	2	US-08-470-335-227	Sequence 227, App	645	150.5	8.3	899	2	US-08-467-602-364	Sequence 364, App
573	150.5	8.3	604	2	US-08-467-602-318	Sequence 318, App	646	150.5	8.3	899	2	US-08-411-295F-290	Sequence 290, App
574	150.5	8.3	604	2	US-08-411-295F-244	Sequence 244, App	647	150.5	8.3	902	2	US-08-467-602-359	Sequence 359, App
575	150.5	8.3	610	2	US-08-470-335-236	Sequence 336, App	648	150.5	8.3	902	2	US-08-411-295F-285	Sequence 285, App
576	150.5	8.3	610	2	US-08-467-602-332	Sequence 332, App	649	150.5	8.3	908	2	US-08-467-602-376	Sequence 376, App
577	150.5	8.3	610	2	US-08-411-295F-258	Sequence 258, App	650	150.5	8.3	908	2	US-08-411-295F-302	Sequence 302, App
578	150.5	8.3	613	2	US-08-470-335-230	Sequence 230, App	651	150.5	8.3	911	2	US-08-467-602-373	Sequence 373, App
579	150.5	8.3	613	2	US-08-467-602-329	Sequence 329, App	652	150.5	8.3	911	2	US-08-411-295F-299	Sequence 299, App
580	150.5	8.3	613	2	US-08-411-295F-255	Sequence 255, App	653	150.5	8.3	922	2	US-08-467-602-367	Sequence 367, App
581	150.5	8.3	624	2	US-08-467-602-326	Sequence 326, App	654	150.5	8.3	922	2	US-08-411-295F-293	Sequence 293, App
582	150.5	8.3	624	2	US-08-411-295F-252	Sequence 252, App	655	150.5	8.3	931	2	US-08-467-602-379	Sequence 379, App
583	150.5	8.3	633	2	US-08-467-602-335	Sequence 335, App	656	150.5	8.3	931	2	US-08-411-295F-305	Sequence 305, App
584	150.5	8.3	633	2	US-08-411-295F-261	Sequence 261, App	657	150.5	8.3	1298	1	US-08-222-616-33	Sequence 33, Appl
585	150.5	8.3	635	2	US-08-467-602-365	Sequence 365, App	658	150.5	8.3	1298	1	US-08-340-011-2	Sequence 2, Appl
586	150.5	8.3	635	2	US-08-411-295F-291	Sequence 291, App	659	150.5	8.3	1298	2	US-08-901-710-2	Sequence 2, Appl
587	150.5	8.3	638	2	US-08-467-602-360	Sequence 360, App	660	150.5	8.3	1298	2	US-08-446-648-33	Sequence 33, Appl
588	150.5	8.3	638	2	US-08-411-295F-286	Sequence 286, App	661	150.5	8.3	1298	2	US-09-982-610-33	Sequence 33, Appl
589	150.5	8.3	644	2	US-08-467-602-374	Sequence 374, App	662	150.5	8.3	1298	2	US-09-169-079-2	Sequence 2, Appl
590	150.5	8.3	644	2	US-08-411-295F-300	Sequence 300, App	663	150.5	8.3	1298	3	US-09-499-468-38	Sequence 38, Appl
591	150.5	8.3	647	2	US-08-467-602-371	Sequence 371, App	664	150.5	8.3	1298	3	US-09-765-534B-2	Sequence 2, Appl
592	150.5	8.3	647	2	US-08-411-295F-297	Sequence 297, App	665	150.5	8.3	1298	3	PCT-US95-04228-33	Sequence 33, Appl
593	150.5	8.3	658	2	US-08-467-602-368	Sequence 368, App	666	150.5	8.3	1362	1	US-08-874-678-33	Sequence 33, Appl
594	150.5	8.3	658	2	US-08-411-295F-294	Sequence 294, App	667	150.5	8.3	1362	1	US-08-643-839-33	Sequence 33, Appl
595	150.5	8.3	667	2	US-08-467-602-377	Sequence 377, App	668	150.5	8.3	1362	2	US-09-348-886-33	Sequence 33, Appl
596	150.5	8.3	667	2	US-08-411-295F-303	Sequence 303, App	669	150.5	8.3	1362	2	US-10-105-901A-33	Sequence 33, Appl
597	150.5	8.3	777	1	US-08-874-678-3	Sequence 3, Appl	670	150.5	8.3	1363	1	US-08-340-011-4	Sequence 4, Appl
598	150.5	8.3	777	2	US-08-643-839-3	Sequence 3, Appl	671	150.5	8.3	1363	2	US-08-901-710-4	Sequence 4, Appl
599	150.5	8.3	777	2	US-09-348-886-3	Sequence 3, Appl	672	150.5	8.3	1363	2	US-09-375-248-2	Sequence 2, Appl
600	150.5	8.3	777	2	US-10-105-901A-3	Sequence 3, Appl	673	150.5	8.3	1363	2	US-09-169-079-4	Sequence 4, Appl
601	150.5	8.3	818	2	US-08-470-335-234	Sequence 234, App	674	150.5	8.3	1363	3	US-09-765-534B-4	Sequence 4, Appl
602	150.5	8.3	818	2	US-08-467-602-321	Sequence 321, App	675	150.5	8.3	1368	1	US-08-874-678-34	Sequence 34, Appl
603	150.5	8.3	818	2	US-08-411-295F-247	Sequence 247, App	676	150.5	8.3	1368	2	US-08-643-839-34	Sequence 34, Appl
604	150.5	8.3	821	2	US-08-470-335-228	Sequence 228, App	677	150.5	8.3	1368	2	US-09-348-886-34	Sequence 34, Appl
605	150.5	8.3	821	2	US-08-467-602-319	Sequence 319, App	678	150.5	8.3	1368	2	US-10-105-901A-34	Sequence 34, Appl
606	150.5	8.3	821	2	US-08-411-295F-245	Sequence 245, App	679	150.5	8.3	355	1	US-08-471-570-14	Sequence 14, Appl
607	150.5	8.3	827	2	US-08-470-335-237	Sequence 237, App	680	150.5	8.3	355	1	US-08-471-570-6	Sequence 6, Appl
608	150.5	8.3	827	2	US-08-467-602-333	Sequence 333, App	681	150.5	8.3	769	1	US-08-471-570-8	Sequence 8, Appl
609	150.5	8.3	827	2	US-08-411-295F-259	Sequence 259, App	682	149.5	8.3	582	3	US-10-162-335-94	Sequence 3, Appl
610	150.5	8.3	830	2	US-08-470-335-231	Sequence 231, App	683	149.5	8.3	1501	1	US-08-447-464-3	Sequence 3, Appl
611	150.5	8.3	830	2	US-08-467-602-330	Sequence 330, App	684	149.5	8.3	1501	1	US-08-716-679-3	Sequence 3, Appl
612	150.5	8.3	830	2	US-08-411-295F-256	Sequence 256, App	685	149.5	8.3	388	1	US-08-429-742-4	Sequence 4, Appl
613	150.5	8.3	830	2	US-08-467-602-327	Sequence 327, App	686	148.5	8.2	1911	1	US-08-348-006B-5	Sequence 5, Appl
614	150.5	8.3	841	2	US-08-411-295F-253	Sequence 253, App	687	148.5	8.2	1911	1	US-08-800-825A-5	Sequence 5, Appl
615	150.5	8.3	850	2	US-08-467-602-336	Sequence 336, App	688	148.5	8.2	1911	2	US-09-158-657-5	Sequence 5, Appl
616	150.5	8.3	850	2	US-08-411-295F-262	Sequence 262, App	689	148.5	8.2	1911	5	PCT-US94-10166-5	Sequence 5, Appl
617	150.5	8.3	852	2	US-08-467-602-363	Sequence 363, App	690	148.5	8.2	602	1	US-08-168-091A-2	Sequence 2, Appl
618	150.5	8.3	852	2	US-08-411-295F-289	Sequence 289, App	691	148.5	8.2	820	1	US-08-166-717D-6	Sequence 6, Appl
619	150.5	8.3	855	2	US-08-467-602-361	Sequence 361, App	692	147.5	8.2	403	2	US-09-638-649-5	Sequence 5, Appl
620	150.5	8.3	855	2	US-08-411-295F-287	Sequence 287, App	693	147.5	8.2	403	2	US-09-638-648-5	Sequence 5, Appl
621	150.5	8.3	861	2	US-08-467-602-375	Sequence 375, App	694	145.5	8.1	252	2	US-09-270-767-4627	Sequence 4627, A
622	150.5	8.3	861	2	US-08-411-295F-301	Sequence 301, App	695	145.5	8.1	549	2	US-09-858-664A-5	Sequence 5, Appl
623	150.5	8.3	864	2	US-08-467-602-372	Sequence 372, App	696	145.5	8.1	549	2	US-10-274-978-6	Sequence 6, Appl
624	150.5	8.3	864	2	US-08-411-295F-298	Sequence 298, App	697	145.5	8.1	549	2	US-10-697-263-6	Sequence 6, Appl
625	150.5	8.3	865	2	US-08-470-335-235	Sequence 235, App	698	145	8.0	972	2	US-08-750-141A-2	Sequence 2, Appl
626	150.5	8.3	865	2	US-08-467-602-322	Sequence 322, App	699	145	8.0	972	2	US-09-944-807-10	Sequence 10, Appl

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705 143 7.9 661 1 US-08-786-164-12 Sequence 12, Appl
706 143 7.9 687 1 US-08-232-538-6 Sequence 6, Appl
707 143 7.9 687 1 US-08-786-164-6 Sequence 6, Appl
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709 142.5 7.9 687 2 US-08-411-295F-77 Sequence 77, Appl
710 142.5 7.9 431 2 US-09-592-998C-9 Sequence 9, Appl
711 142.5 7.9 435 2 US-09-592-998C-10 Sequence 10, Appl
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716 141.5 7.8 257 2 US-08-341-018-6 Sequence 6, Appl
717 141.5 7.8 257 2 US-08-470-339-193 Sequence 193, Appl
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812 138.5 7.7 176 2 US-08-467-602-236 Sequence 236, App
813 138.5 7.7 176 2 US-08-411-295F-162 Sequence 162, App
814 138.5 7.7 196 2 US-08-467-602-244 Sequence 244, App
815 138.5 7.7 196 2 US-08-411-295F-170 Sequence 170, App
816 138.5 7.7 207 2 US-08-467-602-282 Sequence 282, App
817 138.5 7.7 207 2 US-08-411-295F-208 Sequence 208, App
818 138.5 7.7 210 2 US-08-467-602-278 Sequence 278, App
819 138.5 7.7 210 2 US-08-411-295F-204 Sequence 204, App
820 138.5 7.7 230 2 US-08-467-602-286 Sequence 286, App
821 138.5 7.7 230 2 US-08-411-295F-212 Sequence 212, App
822 138.5 7.7 352 2 US-08-467-602-239 Sequence 239, App
823 138.5 7.7 352 2 US-08-411-295F-165 Sequence 165, App
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826 138.5 7.7 361 2 US-08-467-602-248 Sequence 248, App
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828 138.5 7.7 364 2 US-08-467-602-245 Sequence 245, App
829 138.5 7.7 364 2 US-08-411-295F-171 Sequence 171, App
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841 138.5 7.7 398 2 US-08-411-295F-213 Sequence 213, App
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850 138.5 7.7 578 2 US-08-467-602-249 Sequence 249, App
851 138.5 7.7 578 2 US-08-411-295F-175 Sequence 175, App
852 138.5 7.7 581 2 US-08-467-602-246 Sequence 246, App

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855	138.5	7.7	592	2	US-08-411-295F-169	Sequence 169, App	928	134.5	7.4	456	2	US-08-470-335-246	Sequence 246, App
856	138.5	7.7	601	2	US-08-467-602-252	Sequence 252, App	929	134.5	7.4	456	2	US-08-467-602-303	Sequence 303, App
857	138.5	7.7	601	2	US-08-411-295F-178	Sequence 178, App	930	134.5	7.4	456	2	US-08-411-295F-229	Sequence 229, App
858	138.5	7.7	603	2	US-08-467-602-279	Sequence 279, App	931	134.5	7.4	459	2	US-08-470-335-239	Sequence 239, App
859	138.5	7.7	603	2	US-08-411-295F-205	Sequence 205, App	932	134.5	7.4	459	2	US-08-467-602-299	Sequence 299, App
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861	138.5	7.7	606	2	US-08-411-295F-203	Sequence 203, App	934	134.5	7.4	479	2	US-08-467-602-307	Sequence 307, App
862	138.5	7.7	612	2	US-08-467-602-291	Sequence 291, App	935	134.5	7.4	479	2	US-08-411-295F-233	Sequence 233, App
863	138.5	7.7	612	2	US-08-411-295F-217	Sequence 217, App	936	134.5	7.4	490	2	US-08-467-602-345	Sequence 345, App
864	138.5	7.7	615	2	US-08-467-602-288	Sequence 288, App	937	134.5	7.4	490	2	US-08-411-295F-271	Sequence 271, App
865	138.5	7.7	615	2	US-08-411-295F-214	Sequence 214, App	938	134.5	7.4	493	2	US-08-467-602-341	Sequence 341, App
866	138.5	7.7	616	2	US-08-467-602-238	Sequence 238, App	939	134.5	7.4	493	2	US-08-411-295F-267	Sequence 267, App
867	138.5	7.7	616	2	US-08-411-295F-164	Sequence 164, App	940	134.5	7.4	513	2	US-08-467-602-349	Sequence 349, App
868	138.5	7.7	619	2	US-08-467-602-233	Sequence 233, App	941	134.5	7.4	513	2	US-08-411-295F-275	Sequence 275, App
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870	138.5	7.7	625	2	US-08-467-602-250	Sequence 250, App	943	134.5	7.4	534	2	US-08-471-570-4	Sequence 6, Appl
871	138.5	7.7	625	2	US-08-411-295F-176	Sequence 176, App	944	134.5	7.4	534	2	US-09-651-200-6	Sequence 24, Appl
872	138.5	7.7	626	2	US-08-467-602-285	Sequence 285, App	945	134.5	7.4	534	2	US-09-875-338-7	Sequence 7, Appl
873	138.5	7.7	626	2	US-08-411-295F-211	Sequence 211, App	946	134.5	7.4	534	2	US-08-470-335-247	Sequence 247, App
874	138.5	7.7	628	2	US-08-467-602-247	Sequence 247, App	947	134.5	7.4	635	2	US-08-467-602-302	Sequence 302, App
875	138.5	7.7	628	2	US-08-411-295F-173	Sequence 173, App	948	134.5	7.4	635	2	US-08-411-295F-228	Sequence 228, App
876	138.5	7.7	635	2	US-08-467-602-294	Sequence 294, App	949	134.5	7.4	635	2	US-08-470-335-240	Sequence 240, App
877	138.5	7.7	635	2	US-08-411-295F-220	Sequence 220, App	950	134.5	7.4	638	2	US-08-467-602-297	Sequence 297, App
878	138.5	7.7	639	2	US-08-467-602-241	Sequence 241, App	951	134.5	7.4	638	2	US-08-411-295F-223	Sequence 223, App
879	138.5	7.7	639	2	US-08-411-295F-167	Sequence 167, App	952	134.5	7.4	644	5	PCR-US93-00031-19	Sequence 19, Appl
880	138.5	7.7	648	2	US-08-467-602-253	Sequence 253, App	953	134.5	7.4	644	2	US-08-470-335-250	Sequence 250, App
881	138.5	7.7	648	2	US-08-411-295F-179	Sequence 179, App	954	134.5	7.4	644	2	US-08-467-602-311	Sequence 311, App
882	138.5	7.7	650	2	US-08-467-602-280	Sequence 280, App	955	134.5	7.4	644	2	US-08-411-295F-237	Sequence 237, App
883	138.5	7.7	650	2	US-08-411-295F-206	Sequence 206, App	956	134.5	7.4	647	2	US-08-470-335-243	Sequence 243, App
884	138.5	7.7	653	2	US-08-467-602-275	Sequence 275, App	957	134.5	7.4	647	2	US-09-009-490A-91	Sequence 91, Appl
885	138.5	7.7	653	2	US-08-411-295F-201	Sequence 201, App	958	134.5	7.4	647	2	US-08-482-073-5	Sequence 5, Appl
886	138.5	7.7	659	2	US-08-467-602-292	Sequence 292, App	959	134.5	7.4	647	2	US-08-467-602-308	Sequence 308, App
887	138.5	7.7	659	2	US-08-411-295F-218	Sequence 218, App	960	134.5	7.4	647	2	US-08-411-295F-234	Sequence 234, App
888	138.5	7.7	662	2	US-08-467-602-289	Sequence 289, App	961	134.5	7.4	647	2	US-09-982-263C-92	Sequence 92, Appl
889	138.5	7.7	662	2	US-08-411-295F-215	Sequence 215, App	962	134.5	7.4	647	5	PCR-US93-00031-11	Sequence 11, Appl
890	138.5	7.7	673	2	US-08-467-602-283	Sequence 283, App	963	134.5	7.4	647	5	PCR-US93-00031-23	Sequence 23, Appl
891	138.5	7.7	673	2	US-08-411-295F-209	Sequence 209, App	964	134.5	7.4	652	1	US-08-471-570-10	Sequence 10, Appl
892	138.5	7.7	682	2	US-08-467-602-295	Sequence 295, App	965	134.5	7.4	658	2	US-08-467-602-305	Sequence 305, App
893	138.5	7.7	682	2	US-08-411-295F-221	Sequence 221, App	966	134.5	7.4	658	2	US-08-411-295F-231	Sequence 231, App
894	137	7.6	514	2	US-09-949-016-11380	Sequence 11380, A	967	134.5	7.4	667	2	US-08-467-602-314	Sequence 314, App
895	137	7.6	517	2	US-09-723-368-4	Sequence 4, Appl	968	134.5	7.4	667	2	US-08-411-295F-240	Sequence 240, App
896	136.5	7.6	388	1	US-08-443-640-6	Sequence 6, Appl	969	134.5	7.4	669	2	US-08-467-602-344	Sequence 344, App
897	136.5	7.6	388	2	US-08-170-558-6	Sequence 6, Appl	970	134.5	7.4	669	2	US-08-411-295F-270	Sequence 270, App
898	136.5	7.6	388	2	US-08-447-314-6	Sequence 6, Appl	971	134.5	7.4	672	2	US-08-467-602-339	Sequence 339, App
899	136.5	7.6	388	2	US-08-445-461-6	Sequence 6, Appl	972	134.5	7.4	672	2	US-08-411-295F-265	Sequence 265, App
900	136.5	7.6	388	2	US-09-223-490-6	Sequence 6, Appl	973	134.5	7.4	678	2	US-08-467-602-353	Sequence 353, App
901	136.5	7.6	388	3	US-10-646-760-5	Sequence 6, Appl	974	134.5	7.4	678	2	US-08-411-295F-279	Sequence 279, App
902	136.5	7.6	498	2	US-09-354-151-2	Sequence 2, Appl	975	134.5	7.4	681	2	US-08-467-602-350	Sequence 350, App
903	136.5	7.6	738	2	US-08-478-208-32	Sequence 32, Appl	976	134.5	7.4	681	2	US-08-411-295F-276	Sequence 276, App
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905	136.5	7.6	738	7	5264554-2	Patent No. 5264554	978	134.5	7.4	692	2	US-08-411-295F-273	Sequence 273, App
906	136	7.5	393	1	US-08-429-742-2	Sequence 2, Appl	979	134.5	7.4	698	2	US-09-875-338-9	Sequence 9, Appl
907	136	7.5	458	2	US-09-435-956A-1	Sequence 1, Appl	980	134.5	7.4	701	2	US-08-467-602-356	Sequence 356, App
908	136	7.5	644	5	PCR-US93-00031-21	Sequence 21, Appl	981	134.5	7.4	701	2	US-08-411-295F-282	Sequence 282, App
909	135.5	7.5	371	2	US-08-411-295F-308	Sequence 308, App	982	134.5	7.4	740	5	PCR-US93-00031-17	Sequence 17, Appl
910	135.5	7.5	405	2	US-08-467-602-384	Sequence 384, App	983	134.5	7.4	852	2	US-08-470-335-248	Sequence 248, App
911	135.5	7.5	405	2	US-08-411-295F-307	Sequence 307, App	984	134.5	7.4	852	2	US-08-467-602-300	Sequence 300, App
912	135.5	7.5	501	2	US-08-891-845-10	Sequence 10, Appl	985	134.5	7.4	852	2	US-08-411-295F-226	Sequence 226, App
913	135.5	7.5	501	2	US-09-514-573-10	Sequence 10, Appl	986	134.5	7.4	855	2	US-08-470-335-241	Sequence 241, App
914	135.5	7.5	501	2	US-10-290-578-10	Sequence 10, Appl	987	134.5	7.4	855	2	US-08-467-602-298	Sequence 298, App
915	135.5	7.5	768	2	US-08-891-845-2	Sequence 2, Appl	988	134.5	7.4	855	2	US-08-411-295F-224	Sequence 224, App
916	135.5	7.5	768	2	US-09-514-573-2	Sequence 2, Appl	989	134.5	7.4	861	2	US-08-470-335-251	Sequence 251, App
917	135.5	7.5	768	2	US-10-290-578-2	Sequence 2, Appl	990	134.5	7.4	861	2	US-08-467-602-312	Sequence 312, App
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922	135	7.5	525	2	US-09-499-846-8	Sequence 8, Appl	995	134.5	7.4	875	2	US-08-467-602-306	Sequence 306, App
923	134.5	7.4	284	3	US-09-191-651-10	Sequence 10, Appl	996	134.5	7.4	875	2	US-08-411-295F-232	Sequence 232, App
924	134.5	7.4	349	2	US-08-470-335-188	Sequence 188, App	997	134.5	7.4	884	2	US-08-467-602-315	Sequence 315, App
925	134.5	7.4	382	2	US-08-467-602-382	Sequence 382, App	998	134.5	7.4	884	2	US-08-411-295F-241	Sequence 241, App

999	134.5	7.4	886	2	US-08-467-602-342	Sequence 342, App	1089	131.5	7.3	421	3	US-10-162-335-96	Sequence 96, Appl
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1001	134.5	7.4	889	2	US-08-467-602-340	Sequence 340, App	1091	131	7.3	240	1	US-08-471-570-12	Sequence 12, Appl
1002	134.5	7.4	889	2	US-08-411-295F-266	Sequence 266, App	1092	-131	7.3	342	2	US-08-684-708A-27	Sequence 27, Appl
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1005	134.5	7.4	898	2	US-08-467-602-351	Sequence 351, App	1095	131	7.3	1090	2	US-08-866-510-14	Sequence 14, Appl
1006	134.5	7.4	898	2	US-08-411-295F-277	Sequence 277, App	1096	131	7.3	1106	2	US-08-180-195-2	Sequence 2, Appl
1007	134.5	7.4	899	2	US-08-470-335-249	Sequence 249, App	1097	131	7.3	1106	1	US-08-168-917-2	Sequence 2, Appl
1008	134.5	7.4	899	2	US-08-467-602-301	Sequence 301, App	1098	131	7.3	1106	1	US-08-477-329-2	Sequence 2, Appl
1009	134.5	7.4	899	2	US-08-411-295F-227	Sequence 227, App	1099	131	7.3	1106	1	US-08-475-458-2	Sequence 2, Appl
1010	134.5	7.4	902	2	US-08-470-335-242	Sequence 242, App	1100	131	7.3	1106	1	US-08-460-510-2	Sequence 2, Appl
1011	134.5	7.4	902	2	US-08-467-602-296	Sequence 296, App	1101	131	7.3	1106	1	US-08-460-490-2	Sequence 2, Appl
1012	134.5	7.4	902	2	US-08-411-295F-222	Sequence 222, App	1102	131	7.3	1106	2	US-08-980-400-2	Sequence 2, Appl
1013	134.5	7.4	908	2	US-08-470-335-252	Sequence 252, App	1103	131	7.3	1106	2	US-08-462-728-4	Sequence 4, Appl
1014	134.5	7.4	908	2	US-08-467-602-313	Sequence 313, App	1104	131	7.3	1106	2	US-09-583-459A-2	Sequence 2, Appl
1015	134.5	7.4	908	2	US-08-411-295F-239	Sequence 239, App	1105	131	7.3	1106	2	US-09-583-210-2	Sequence 2, Appl
1016	134.5	7.4	909	2	US-08-467-602-348	Sequence 348, App	1106	131	7.3	1106	2	US-09-583-449A-2	Sequence 2, Appl
1017	134.5	7.4	909	2	US-08-411-295F-274	Sequence 274, App	1107	131	7.3	1106	2	US-09-435-059-2	Sequence 2, Appl
1018	134.5	7.4	911	2	US-08-470-335-245	Sequence 245, App	1108	131	7.3	1106	2	US-08-461-917-4	Sequence 4, Appl
1019	134.5	7.4	911	2	US-08-467-602-310	Sequence 310, App	1109	131	7.3	1106	2	US-08-464-436-4	Sequence 4, Appl
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1032	134.5	7.4	942	2	US-08-411-295F-281	Sequence 281, App	1122	130.5	7.2	315	2	US-09-949-016-11121	Sequence 11121, A
1033	134.5	7.4	945	2	US-08-467-602-352	Sequence 352, App	1123	130.5	7.2	315	2	US-09-949-016-11122	Sequence 11122, A
1034	134.5	7.4	945	2	US-08-411-295F-278	Sequence 278, App	1124	130.5	7.2	432	2	US-08-477-460B-2	Sequence 2, Appl
1035	134.5	7.4	956	2	US-08-467-602-346	Sequence 346, App	1125	130.5	7.2	432	2	US-08-379-516-2	Sequence 2, Appl
1036	134.5	7.4	956	2	US-08-411-295F-272	Sequence 272, App	1126	130.5	7.2	432	2	US-09-329-916-2	Sequence 2, Appl
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1052	133	7.4	612	1	US-08-286-846A-8	Sequence 8, Appl	1142	128.5	7.1	421	3	US-10-162-335-100	Sequence 100, App
1053	133	7.4	612	1	US-08-457-880A-8	Sequence 8, Appl	1143	128	7.1	341	2	US-09-336-536-29	Sequence 29, Appl
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1056	133	7.4	612	2	US-09-156-923-8	Sequence 8, Appl	1146	128	7.1	483	2	US-09-166-750-19	Sequence 19, Appl
1057	133	7.4	816	2	US-09-949-016-10904	Sequence 10904, A	1147	128	7.1	483	2	US-09-166-093-19	Sequence 19, Appl
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1061	133	7.4	839	2	US-08-444-622A-6	Sequence 6, Appl	1151	128	7.1	483	2	US-09-443-213-19	Sequence 19, Appl
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1069	132	7.3	408	2	US-09-724-864-62	Sequence 62, Appl	1159	127.5	7.1	206	2	US-08-411-295F-76	Sequence 76, Appl
1070	131.5	7.3	312	2	US-09-254-465A-9	Sequence 9, Appl	1160	127.5	7.1	206	2	US-08-411-295F-94	Sequence 94, Appl
1080	131.5	7.3	312	2	US-09-953-499-9	Sequence 9, Appl	1161	127.5	7.1	241	2		

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1164	127.5	7.1	447	2	US-09-949-016-8211	Sequence 8211, Ap	Sequence 8211, Ap	1248	123.5	6.8	156	2	US-08-467-602-381	Sequence 381, App
1165	127	7.0	383	2	US-09-949-016-11050	Sequence 11050, A	Sequence 11050, A	1249	123.5	6.8	156	2	US-08-411-295F-306	Sequence 306, Appl
1166	127	7.0	917	2	US-10-282-162-54	Sequence 54, Appl	Sequence 54, Appl	1250	123.5	6.8	241	1	US-07-847-743B-30	Sequence 30, Appl
1167	127	7.0	917	2	US-10-282-162-56	Sequence 56, Appl	Sequence 56, Appl	1251	123.5	6.8	241	1	US-08-456-201-30	Sequence 30, Appl
1168	127	7.0	992	1	US-07-813-593-2	Sequence 2, Appli	Sequence 2, Appli	1252	123.5	6.8	241	5	PCT-US92-04295A-30	Sequence 30, Appl
1169	127	7.0	992	1	US-07-977-451-2	Sequence 2, Appli	Sequence 2, Appli	1253	123.5	6.8	241	5	PCT-US92-04295A-30	Sequence 30, Appl
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1171	127	7.0	992	1	US-08-252-517-2	Sequence 2, Appli	Sequence 2, Appli	1255	123.5	6.8	420	1	US-07-847-743B-29	Sequence 29, Appl
1172	127	7.0	992	1	US-07-906-397A-2	Sequence 2, Appli	Sequence 2, Appli	1256	123.5	6.8	420	1	US-08-456-201-29	Sequence 29, Appl
1173	127	7.0	992	1	US-08-601-891-2	Sequence 2, Appli	Sequence 2, Appli	1257	123.5	6.8	420	1	US-08-456-241-29	Sequence 29, Appl
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1177	127	7.0	992	5	PCT-US92-02750-2	Sequence 2, Appli	Sequence 2, Appli	1261	123.5	6.8	637	1	US-08-456-241-28	Sequence 28, Appl
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1182	126.5	7.0	365	2	US-09-949-016-6064	Sequence 6064, Ap	Sequence 6064, Ap	1266	123.5	6.8	645	1	US-08-428-927-4	Sequence 4, Appli
1183	126.5	7.0	365	2	US-09-354-151-3	Sequence 3, Appli	Sequence 3, Appli	1267	123.5	6.8	645	1	US-08-428-298-4	Sequence 4, Appli
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 1337 122.5 6.8 603 2 US-08-411-295F-142 Sequence 142, App
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 1482 119.5 6.6 477 2 US-09-949-016-9194 Sequence 9194, Ap
 1483 119.5 6.6 477 2 US-09-949-016-9195 Sequence 9195, Ap
 1484 119.5 6.6 477 2 US-09-949-016-9196 Sequence 9196, Ap
 1485 119.5 6.6 477 2 US-09-949-016-9197 Sequence 9197, Ap
 1486 119.5 6.6 477 2 US-09-949-016-9198 Sequence 9198, Ap
 1487 119.5 6.6 477 2 US-09-949-016-9199 Sequence 9199, Ap
 1488 119.5 6.6 505 2 US-09-240-915-3 Sequence 3, Appl
 1489 119.5 6.6 505 2 US-09-581-435-3 Sequence 3, Appl
 1490 119.5 6.6 505 2 US-10-098-600B-3 Sequence 3, Appl
 1491 119 6.6 261 2 US-09-899-634C-2 Sequence 2, Appl
 1492 119 6.6 330 1 US-08-525-864A-4 Sequence 4, Appl
 1493 119 6.6 365 2 US-09-899-634C-4 Sequence 4, Appl
 1494 119 6.6 754 1 US-08-525-864A-2 Sequence 2, Appl
 1495 119 6.6 910 2 US-09-313-942-28 Sequence 28, Appl
 1496 119 6.6 910 2 US-10-282-162-48 Sequence 28, Appl
 1497 119 6.6 969 2 US-09-949-016-8059 Sequence 8059, Ap
 1498 118.5 6.6 553 1 US-08-263-911-7 Sequence 7, Appl
 1499 118.5 6.6 668 2 US-09-949-016-8139 Sequence 8139, Ap
 1500 118.5 6.6 931 2 US-10-037-417-118 Sequence 118, App

ALIGNMENTS


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RESULT 1
US-09-700-397-3
; Sequence 3, Application US/09700397
; Patent No. 6664383
; GENERAL INFORMATION:
; APPLICANT: Onco Pharmaceutical Co., Ltd.
; TITLE OF INVENTION: No. 6664383el Polypeptides, cDNA encoding the same, and use of
; FILE REFERENCE: Q61459
; CURRENT APPLICATION NUMBER: US/09/700,397
; CURRENT FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: JP 10-131815
; PRIOR FILING DATE: 1998-05-14
; PRIOR APPLICATION NUMBER: PCT/JP99/02485
; PRIOR FILING DATE: 1999-05-13
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 344
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Clone OC001 derived from human brain
US-09-700-397-3

Query Match      100.0%; Score 1806; DB 2; Length 344;
Best Local Similarity 100.0%; Pred. No. 3.3e-172;
Matches 344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      181  SEDSYLEIQITREQSGDYCSASNDVAAPVVRVKVTNVPYVPISEAKGTGVPVGQKGT 240
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Qy      301  LGHTNASIMLFGPGAVSEVSGTSTRRAGCVWLLPLLVHLHLKLF 344
Db      301  LGHTNASIMLFGPGAVSEVSGTSTRRAGCVWLLPLLVHLHLKLF 344

RESULT 2
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; Patent No. 6916648
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Deenoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
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; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
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; APPLICANT: Hillan, Kenneth J
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630PIC65
; CURRENT APPLICATION NUMBER: US/09/999,833A
; CURRENT FILING DATE: 2001-10-24
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
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; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Query Match 100.0%; Score 1806; DB 2; Length 344;

Best Local Similarity 100.0%; Pred. No. 3.3e-172; Indels 0; Gaps 0;
Matches 344; Conservative 0; Mismatches 0

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Qy 121 NHPKTSRVHLIVQVSPKIVEISSDISINEGNNISLTCTIATGRPEPTVTVRHI SPKAVGFV 180
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Qy 181 SEDEYLEIQITREQSGDYECASNDVAAPVVRVKVTVVNPYPISEAKGTGVPVGQKGT 240
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Qy 241 LQCEASAVPSAEPQWYKDDKRLIEGKGVKVENPFLSKLIFNVSEHDYNYTCVASNK 300
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RESULT 3

; Sequence 523, Application US/10020445A
; Patent No. 6962797
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David

APPLICANT: Deenoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerriksen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630P1C74
CURRENT APPLICATION NUMBER: US/10/020,445A
CURRENT FILING DATE: 2001-10-24
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 60/052250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/054249
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;	PRIOR APPLICATION NUMBER:	60/085697	

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Qy 301 LGHTNASIMLPGCAVSEVSGTSSRAGCCWMLPLVLVHLLK 344
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RESULT 4
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; Patent No. 6972325
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kijavlin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C7
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; CURRENT FILING DATE: 2001-10-15
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; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Query Match 100.0%; Score 1806; DB 2; Length 344;
Best Local Similarity 100.0%; Pred. No. 3.3e-172;
Matches 344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKTIQPKMNSISWALFTGLAALCLFQGVVRSGLATFPKAMDNVTVRQGESATLRCTID 60
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Db 1 MKTIQPKMNSISWALFTGLAALCLFQGVVRSGLATFPKAMDNVTVRQGESATLRCTID 60
|||||

Qy 61 NRVTRVAVLNRSTILYAGNDKWCCLDRPVVLLSNTQTQYSIEIQNDVYDEGPTCSVQTD 120
|||||

Db 61 NRVTRVAVLNRSTILYAGNDKWCCLDRPVVLLSNTQTQYSIEIQNDVYDEGPTCSVQTD 120
|||||

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Db	121	NHPKTSRVHLIVQVSPKIVEISSDISEGNNISLTCIATGRPPTVTWRIISPKAVGFV	180
Qy	181	SEDEYLEIIGITIREQSGDYECASNDVAAPVVRVKVTNVPPIYSEAKGTGVPVGQGT	240
Db	181	SEDEYLEIIGITIREQSGDYECASNDVAAPVVRVKVTNVPPIYSEAKGTGVPVGQGT	240
Qy	241	LQCEASAVPSAEFQWKDDKRLIEGKGVKVENRPFSLKLIFFNVSEHDYGNVTCVASNK	300
Db	241	LQCEASAVPSAEFQWKDDKRLIEGKGVKVENRPFSLKLIFFNVSEHDYGNVTCVASNK	300
Qy	301	LGHNASIMLPGGAVSEVNGTSRRAGCWMLLPLLVLHLHLKLF	344
Db	301	LGHNASIMLPGGAVSEVNGTSRRAGCWMLLPLLVLHLHLKLF	344

RESULT 5
: Sequence 523, Application US/10017085A

: GENERAL INFORMATION:

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, APPLICANT: Ashkenazi, Avi
, APPLICANT: Baker, Kevin P.
, APPLICANT: Botstein, David
, APPLICANT: Desnovers, Luc
, APPLICANT: Eaton, Dan
, APPLICANT: Ferrara, Napoleon
, APPLICANT: Flivaroff, Ellen
, APPLICANT: Fong, Sherman
, APPLICANT: Gao, Wei-Qiang
, APPLICANT: Gerber, Hanspeter
, APPLICANT: Gerritsen, Mary E.
, APPLICANT: Goddard, Audrey
, APPLICANT: Godowski, Paul J.
, APPLICANT: Grimaldi, J. Christopher
, APPLICANT: Gurney, Austin L.
, APPLICANT: Hillan, Kenneth J
, APPLICANT: Kijavlin, Ivar J.
, APPLICANT: Kuo, Sophia S.
, APPLICANT: Napier, Mary A.
, APPLICANT: Pan, James;
, APPLICANT: Paoni, Nicholas F.
, APPLICANT: Roy, Margaret Ann
, APPLICANT: Shelton, David L.
, APPLICANT: Stewart, Timothy A.
, APPLICANT: Tumas, Daniel
, APPLICANT: Williams, P. Mickey
, APPLICANT: Wood, William I.
, TITLE OF INVENTION: Secreted and Tra
, TITLE OF INVENTION: Acids Encoding
, FILE REFERENCE: P2630P1C73
, CURRENT APPLICATION NUMBER: US/10/01
, CURRENT FILING DATE: 2002-04-30
, Prior Application removed - File Wra
, NUMBER OF SEQ ID NOS: 624
, SEQ ID NO 523
, LENGTH: 344
, TYPE: PRT
, ORGANISM: Homo sapiens

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RESULT 6

RESOLUTION 8
; Sequence 523, Application US/10145129A
; Patent No. 7019115

: GENERAL INFORMATION:

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> APPLICANT: Ashkenazi, Avi
> APPLICANT: Baker Kevin P.
> APPLICANT: Botstein, David
> APPLICANT: Desnoyers, Luc
> APPLICANT: Eaton, Dan
> APPLICANT: Ferrara, Napoleon
> APPLICANT: Filvaroff, Ellen
> APPLICANT: Fong, Sherman
> APPLICANT: Gao, Wei-Qiang
> APPLICANT: Gerber, Hanspeter
> APPLICANT: Gerritsen, Mary E.
> APPLICANT: Goddard, Audrey
> APPLICANT: Godowski, Paul J.
> APPLICANT: Grimaldi, J. Christopher
> APPLICANT: Gurney, Austin L.
> APPLICANT: Hillan, Kenneth J.
> APPLICANT: Kljavin, Ivar J.
> APPLICANT: Kuo, Sophia S.
> APPLICANT: Napier, Mary A.
> APPLICANT: Pan, James;
> APPLICANT: Paoni, Nicholas F.
> APPLICANT: Roy, Margaret Ann
> APPLICANT: Shelton, David L.
> APPLICANT: Stewart, Timothy A.
> APPLICANT: Tumas, Daniel
> APPLICANT: Williams, P. Mickey
> APPLICANT: Wood, William I.
> TITLE OF INVENTION: Acids and Transmembrane Polypeptides and Nucleic
> TITLE OF INVENTION: Acids Encoding the Same
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> CURRENT APPLICATION NUMBER: US/10/145,129A
> CURRENT FILING DATE: 2002-10-10
> PRIOR APPLICATION NUMBER: 09/918585
> PRIOR FILING DATE: 2001-07-30
> PRIOR APPLICATION NUMBER: 60/062250
> PRIOR FILING DATE: 1997-10-17
> PRIOR APPLICATION NUMBER: 60/064249
> PRIOR FILING DATE: 1997-11-03
> PRIOR APPLICATION NUMBER: 60/065311
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> Remaining Prior Application data removed - See File wrapper or PALM.

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; NUMBER OF SEQ ID NOS: 624
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; ORGANISM: Homo sapiens

Query Match
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RESULT 7
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; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
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; APPLICANT: Eaton, Dan
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; APPLICANT: Filvaroff, Ellen
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; APPLICANT: Gao, Wei-Qiang
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; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
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; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085573
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Query Match 100.0%; Score 1806; DB 3; Length 344;
Best Local Similarity 100.0%; Pred. No. 3.3e-172;
Matches 344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MKTIQPKMHSISWAIFTGLAALCLFQGVPRVSGDATPPKAMDNVTVRQGESATILRCTID 60
Db 1 MKTIQPKMHSISWAIFTGLAALCLFQGVPRVSGDATPPKAMDNVTVRQGESATILRCTID 60
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Qy 241 LQCEASAVPSAEFQWYKDDKRLIEGKGVKVENPFSLKLIFFNVSEHDYGNITCVASNK 300
Db 241 LQCEASAVPSAEFQWYKDDKRLIEGKGVKVENPFSLKLIFFNVSEHDYGNITCVASNK 300
Qy 301 LGHTNASIMLFGPGAVSEVSNGTSSRRAGCVWLLPLLVHLHLKF 344
Db 301 LGHTNASIMLFGPGAVSEVSNGTSSRRAGCVWLLPLLVHLHLKF 344

RESULT 8

; Sequence 523, Application US/10013917A

; Patent No. 7029874

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi

; APPLICANT: Baker Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan

; APPLICANT: Ferrara, Napoleon

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Fong, Sherman

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Gerber, Hanspeter

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, J. Christopher

; APPLICANT: Gurney, Austin L.

; APPLICANT: Hillan, Kenneth J.

; APPLICANT: Kljavin, Ivar J.

; APPLICANT: Kuo, Sophia S.

; APPLICANT: Napier, Mary A.

; APPLICANT: Pan, James

; APPLICANT: Paoni, Nicholas F.

; APPLICANT: Roy, Margaret Ann

APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630P1C82
CURRENT APPLICATION NUMBER: US/10/013.917A
CURRENT FILING DATE: 2001-10-25
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 624
SEQ ID NO 523
LENGTH: 344
TYPE: PRT
ORGANISM: Homo sapiens

Query Match 100.0%; Score 1806; DB 3; Length 344;
Best Local Similarity 100.0%; Pred. No. 3.3e-172; Indels 0; Gaps 0;
Matches 344; Conservative 0; Mismatches 0;

Qy 1 MKTIQPKHNSISWAIETGLAALCLFQGVPRSGDATFPKAMDNVTVRQGESATLRCTID 60
Db 1 MKTIQPKHNSISWAIETGLAALCLFQGVPRSGDATFPKAMDNVTVRQGESATLRCTID 60

Qy 61 NRVTRVAVLNRSTLYAGNDKWCCLDPRVLLSNTQTOYSIEIQNVVDVDEGPTCSVQTD 120
Db 61 NRVTRVAVLNRSTLYAGNDKWCCLDPRVLLSNTQTOYSIEIQNVVDVDEGPTCSVQTD 120

Qy 121 NHPKTSRVHLIVQSPKIVEISSDISINEGNSISLTCTIATGRPEPTVTRHISPKAVGFV 180
Db 121 NHPKTSRVHLIVQSPKIVEISSDISINEGNSISLTCTIATGRPEPTVTRHISPKAVGFV 180

Qy 181 SEDEYLEIQITRQSGDYECSSASNDVAAPVRRVKVTNNPPYISEAKGTGVPVGQKGT 240
Db 181 SEDEYLEIQITRQSGDYECSSASNDVAAPVRRVKVTNNPPYISEAKGTGVPVGQKGT 240

Qy 241 LQCEASAVPSAEFQWYKDDKRLIEGKGVKVENRPFSLKLIFFNVSEHDYGNVTCVASNK 300
Db 241 LQCEASAVPSAEFQWYKDDKRLIEGKGVKVENRPFSLKLIFFNVSEHDYGNVTCVASNK 300

Qy 301 LGHTNASIMLFGPCAVSEVNGTSRRAGCVMWLLPLLVHLLKF 344
Db 301 LGHTNASIMLFGPCAVSEVNGTSRRAGCVMWLLPLLVHLLKF 344

RESULT 9
US-09-700-397-4
; Sequence 4, Application US/09700397
; Patent No. 6664383
; GENERAL INFORMATION:
; APPLICANT: Ono Pharmaceutical Co., Ltd.
; TITLE OF INVENTION: No. 6664383el Polypeptides, cDNA encoding the same, and use of
; FILE REFERENCE: 061459
; CURRENT APPLICATION NUMBER: US/09/700.397
; CURRENT FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: JP 10-131815
; PRIOR FILING DATE: 1998-05-14
; PRIOR APPLICATION NUMBER: PCT/JP99/02485
; PRIOR FILING DATE: 1999-05-13
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 4
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-700-397-4

Query Match 90.9%; Score 1642; DB 2; Length 313;
Best Local Similarity 100.0%; Pred. No. 7.5e-156;
Matches 313; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 32 RSGDATFPKAMDNVTVRQGESATLRCTIDNRVTRVAVLNRSTLYAGNDKWCCLDPRVLL 91

Db 1 RSGDATFPKAMDNVTVRQGESATLRCTIDNRVTRVAVLNRSTLYAGNDKWCCLDPRVLL 60

Qy 92 SNTQTOYSIEIQNVVDVDEGPTCSVQTDNHPKTSRVHLIVQSPKIVEISSDISINEGN 151
Db 61 SNTQTOYSIEIQNVVDVDEGPTCSVQTDNHPKTSRVHLIVQSPKIVEISSDISINEGN 120

Qy 152 NISLTCTIATGRPEPTVTRHISPKAVGFVSEDEYLEIQITRQSGDYECSSASNDVAAPV 211
Db 121 NISLTCTIATGRPEPTVTRHISPKAVGFVSEDEYLEIQITRQSGDYECSSASNDVAAPV 180

Qy 212 VRRVKVTNNPPYISEAKGTGVPVGQKGTQCEASAVPSAEFQWYKDDKRLIEGKGVKV 271
Db 181 VRRVKVTNNPPYISEAKGTGVPVGQKGTQCEASAVPSAEFQWYKDDKRLIEGKGVKV 240

Qy 272 ENRPFLSKLIFFNVSEHDYGNVTCVASNKLGHTNASIMLFGPCAVSEVNGTSRRAGCVM 331
Db 241 ENRPFLSKLIFFNVSEHDYGNVTCVASNKLGHTNASIMLFGPCAVSEVNGTSRRAGCVM 300

Qy 332 LPLLVHLLKF 344
Db 301 LPLLVHLLKF 313

RESULT 10
US-09-976-594-404
; Sequence 404, Application US/09976594
; Patent No. 6673549
; GENERAL INFORMATION:
; APPLICANT: Furness, Michael
; APPLICANT: Buchbinder, Jenny
; TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
; FILE REFERENCE: PA-0041 US
; CURRENT APPLICATION NUMBER: US/09/976.594
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/240.409
; PRIOR FILING DATE: 2000-10-12
; NUMBER OF SEQ ID NOS: 1143
; SOFTWARE: PERL Program
; SEQ ID NO 404
; LENGTH: 338
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6673549 1640555CD1
US-09-976-594-404

Query Match 51.6%; Score 931.5; DB 2; Length 338;
Best Local Similarity 55.4%; Pred. No. 1.2e-84;
Matches 180; Conservative 60; Mismatches 80; Indels 5; Gaps 4;

Qy 20 LAALCLF-QGVPRVSGDATFPKAMDNVTVRQGESATLRCTIDNRVTRVAVLNRSTLYAG 78
Db 17 LRLLCLLPTGLPVRVD--FNRGTDNITVRQGTALRCLVEDKSKVAVLNRSGIIFAG 74

Qy 79 NDKWCCLDPRVLLSNTQTOYSIEIQNVVDVDEGPTCSVQTDNHPKTSRVHLIVQSPKI 138
Db 75 HDKWCCLDPRVELEKSRHSLEYSRIQVDVDEGPTCSVQTDNHPKTSRVHLIVQSPKI 134

Qy 139 VEISSDISINEGNSISLTCTIATGRPEPTVTRHISPKAVGFVSEDEYLEIQITRQSGD 198
Db 135 SNISSDVTNVEGNSVTLVCMANGRPPEPTVTRHISPKAVGFVSEDEYLEIQITRQSGK 194

Qy 199 YECASNDVAAPVRRVKVTNNPPYISEAKGTGVPVGQKGTQCEASAVPSAEFQWYK 258
Db 195 YECKAANEVSSADVQKVTVNPPYITTSKSNSEATTGQASLKCEASAVPADFEWYRD 254

Qy 259 DKRLIEGKGVKVENRPFSLKLIFFNVSEHDYGNVTCVASNKLGHTNASIMLFGPCAVSE 318
Db 255 DTR-INSANGLEIKSTEGQSSLTVTNVTBEHYGNVTCVAANKLGVTNASLVLFRPGSVRG 313

Qy 319 VSGTSRRAGCVMWLLPLLVHLLKF 343

[illegible]

QY 259 DKRLIEGKGVKVENRPFSLKLIFFNVSEHDYGYNTCVASNKLGHTNASIMLFGPGAVSE 318
DB 255 DTR-INSANGLEIKSTEGOSSLTVTNVTBHHYGYNTCVAAANKLGVTNASLVLFPRGSGVRG 313
QY 319 VSGTSTRRAGCVWLLPLLVHLHLK 343
DB 314 I-NGSISLAVPLWLLAASUFLCLSK 337

RESULT 13
US-09-135-080-4
; Sequence 4, Application US/09135080
; Patent No. 6423827
; GENERAL INFORMATION:
; APPLICANT: Levitt, Pat R.
; APPLICANT: Pimenta, Aurea
; APPLICANT: Fischer, Itzhak
; APPLICANT: Zhukareva, Victoria
; TITLE OF INVENTION: Limbic System-Associated Membrane
; TITLE OF INVENTION: Protein and DNA
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dechert Price & Rhoads
; STREET: 997 Lenox Drive, Building 3, Suite 210
; CITY: Lawrenceville
; STATE: NJ
; COUNTRY: USA
; ZIP: 08543
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09135,080
; FILING DATE: 17-AUG-1998
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/414,657
; FILING DATE: 31-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Bloom, Allen
; REGISTRATION NUMBER: 29,135
; REFERENCE/DOCKET NUMBER: 317743-102A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609-620-3214
; TELEFAX: 609-620-3259
; TELEX:
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 338 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-135-080-4

Query Match 51.3%; Score 926.5; DB 2; Length 338;
Best Local Similarity 55.1%; Pred. No. 4e-84;
Matches 179; Conservative 60; Mismatches 81; Indels 5; Gaps 4;

QY 20 LAALCLF-QGVPRSGDATFPKAMDNTVVRQGESATLRCTIDNRVTRVAWLNRSITLYAG 78
DB 17 LRLCLLPTGLPVRSD--FNRGTDNITVRQGDITAILRCVLEDKNSKVAVLNRSIGIFAG 74

QY 79 NDKWCLDPRVLLSNTQYISIEIQNVVDYDEGPTCSVOTDNHPKTSRVHLIVQVSPKI 138
DB 75 HDKWSLDPVLEKXHALEYSLRIQKVDYDEGPTCSVOTQHEPKTSQVYLIVQVPPKI 134

QY 139 VEISSDTSINEGNNISLTATGRPEPTVTRWHISPKAVGVFSEDEYLEIQGITREQSGD 198
DB 135 SNISSDVTVNEGSNVLVLCVANGRPEPTVTRHLTPLGREFEGEEYLEILGITREQSGK 194

QY 199 YECASNDVAAPVRRVKTVTVNPPYISEAKGTGVPVQKGTLOCEASAVPSABEQWYKD 258
DB 195 YECKAANEVSSADVQKVQVTVNPPYITTESKNEATTGROASLKCEASAVPAPDEFWYRD 254
QY 259 DKRLIEGKGVKVENRPFSLKLIFFNVSEHDYGYNTCVASNKLGHTNASIMLFGPGAVSE 318
DB 255 DTR-INSANGLEIKSTEGOSSLTVTNVTBHHYGYNTCVAAANKLGVTNASLVLFPRGSGVRG 313
QY 319 VSGTSTRRAGCVWLLPLLVHLHLK 343
DB 314 I-NGSISLAVPLWLLAASUFLCLSK 337

RESULT 14
US-08-414-657D-2
; Sequence 2, Application US/08414657D
; Patent No. 5861283
; GENERAL INFORMATION:
; APPLICANT: Levitt, Pat
; APPLICANT: Pimenta, Aurea
; APPLICANT: Fischer, Itzhak
; APPLICANT: Zhukareva, Victoria
; TITLE OF INVENTION: Limbic System-Associated Membrane
; TITLE OF INVENTION: Protein and DNA
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dechert Price & Rhoads
; STREET: 997 Lenox Drive, Building 3, Suite 210
; CITY: Lawrenceville
; STATE: NJ
; COUNTRY: USA
; ZIP: 08543
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08414,657D
; FILING DATE: 31-MAR-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Bloom, Allen
; REGISTRATION NUMBER: 29,135
; REFERENCE/DOCKET NUMBER: 317743-102
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609-520-3214
; TELEFAX: 609-520-3259
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 325 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
; US-08-414-657D-2

Query Match 51.1%; Score 923.5; DB 1; Length 325;
Best Local Similarity 55.3%; Pred. No. 7.4e-84;
Matches 177; Conservative 60; Mismatches 78; Indels 5; Gaps 4;

QY 20 LAALCLF-QGVPRSGDATFPKAMDNTVVRQGESATLRCTIDNRVTRVAWLNRSITLYAG 78
DB 10 LRLCLLPTGLPVRSD--FNRGTDNITVRQGDITAILRCVLEDKNSKVAVLNRSIGIFAG 67

QY 79 NDKWCLDPRVLLSNTQYISIEIQNVVDYDEGPTCSVOTDNHPKTSRVHLIVQVSPKI 138
DB 68 HDKWSLDPVLEKXHALEYSLRIQKVDYDEGPTCSVOTQHEPKTSQVYLIVQVPPKI 127

QY 139 VEISSDISINEGNISLTCTIATGRPEPTVTRHISPKAVGFVSEDEYLEIOGITREOSGD 198
Db 128 SNISSDVTNEGNSVTLVCMANGREPVTWRHLTPTGREFEGBEYLEILGITREOSGK 187
QY 199 YECASNDVAAPVRRVKVTYVPPYISBAKGTGVPVGQKGTLOCEASAVPSAEFQWYKD 258
Db 188 YECCAANEVSSADVQKVTVNPPYITTESKNEATTGROASLKCEASAVPAPDFEYRD 247
QY 259 DKRLTEGKGVKVENRPFSLKLIFFENVSEHDYGNVTCVASNKLGHNTNASIMLFGPCAVSE 318
Db 248 DTR-INSANGLEIKSTEGOSSLTVTNVTTEEYGNVTCVAANKLGVTNASLVLFPRGVSVRG 306
QY 319 VSGTSTRRAGCVWLLPLLV 338
Db 307 I-NGSISLAVPLWLLAASLL 325

RESULT 15
US-08-414-657D-41
; Sequence 41, Application US/08414657D
; Patent No. 5861283
; GENERAL INFORMATION:
; APPLICANT: Levitt, Pat
; APPLICANT: Pimental, Aurea
; APPLICANT: Fischer, Itzhak
; APPLICANT: Zhukareva, Victoria
; TITLE OF INVENTION: Limbic System-Associated Membrane
; TITLE OF INVENTION: Protein and DNA
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dechert Price & Rhoads
; STREET: 997 Lenox Drive, Building 3, Suite 210
; CITY: Lawrenceville
; STATE: NJ
; COUNTRY: USA
; ZIP: 08543
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/414,657D
; FILING DATE: 31-MAR-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Bloom, Allen
; REGISTRATION NUMBER: 29,135
; REFERENCE/DOCKET NUMBER: 317743-102
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609-520-3214
; TELEFAX: 609-520-3259
; TELEX:
; INFORMATION FOR SEQ ID NO: 41:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 325 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-414-657D-41

Query Match 51.1%; Score 923.5; DB 1; Length 325;
Best Local Similarity 55.3%; Pred. No. 7 4e-84;
Matches 177; Conservative 60; Mismatches 78; Indels 5; Gaps 4;
QY 20 LAALCLF-QGVPRSGDATFPKAMDNVTYRQGESATLRCITDNRVTRVAVLNRSTLYAG 78
Db 10 LRLCLLPTGLPVRSD--FNRGTDNITVRQGDITAILRCVLEDKNSKVAVLNRSGIIFAG 67

QY 79 NDKWLCDPRVLLSNTQYSEIQNVVDYDEGPTVCSVQTDNHPKTSRVHLIVQVSPKI 138
Db 68 HDKWSLDRVELEKEHSLSEYSLRIOKVDYDEGPTVCSVQTCHEPKTSQVYLIVQVPPKI 127
QY 139 VEISSDISINEGNISLTCTIATGRPEPTVTRHISPKAVGFVSEDEYLEIOGITREOSGD 198
Db 128 SNISSDVTNEGNSVTLVCMANGREPVTWRHLTPTGREFEGBEYLEILGITREOSGK 187
QY 199 YECASNDVAAPVRRVKVTYVPPYISBAKGTGVPVGQKGTLOCEASAVPSAEFQWYKD 258
Db 188 YECCAANEVSSADVQKVTVNPPYITTESKNEATTGROASLKCEASAVPAPDFEYRD 247
QY 259 DKRLTEGKGVKVENRPFSLKLIFFENVSEHDYGNVTCVASNKLGHNTNASIMLFGPCAVSE 318
Db 248 DTR-INSANGLEIKSTEGOSSLTVTNVTTEEYGNVTCVAANKLGVTNASLVLFPRGVSVRG 306
QY 319 VSGTSTRRAGCVWLLPLLV 338
Db 307 I-NGSISLAVPLWLLAASLL 325

Search completed: October 21, 2006, 18:06:42
Job time : 64 secs

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GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: October 21, 2006, 18:11:16 Search time 75 Seconds
(without alignments)
2124.612 Million cell updates/sec

Perfect score: 1806
Sequence: 1 MKTIQPKMHSISWAIFGL.....RRAGCVMLPLLVLLHLLKF 344

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

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2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
52	1806	100.0	344	4	US-10-066-269-104
64	1806	100.0	344	4	US-10-167-749-523
226	1806	100.0	344	4	US-10-223-085-56
232	1806	100.0	344	4	US-10-219-065-126
262	1806	100.0	344	4	US-10-223-084-56
263	1806	100.0	344	4	US-10-223-088-56
264	1806	100.0	344	4	US-10-223-090-56
271	1806	100.0	344	4	US-10-223-087-56
274	1806	100.0	344	4	US-10-223-083-56
447	1806	100.0	344	4	US-10-223-089-56
485	1806	100.0	344	4	US-10-223-081-56
554	1806	100.0	344	4	US-10-223-082-56
556	1806	100.0	344	4	US-10-170-481A-523
613	1806	100.0	344	4	US-10-210-028-523
623	1806	100.0	344	4	US-10-162-521A-523
625	1806	100.0	344	4	US-10-305-654-56
635	1806	100.0	344	4	US-10-657-103-3
639	1806	100.0	344	4	US-10-081-056-56
659	1806	100.0	344	5	US-10-918-851-523
660	1806	100.0	344	5	US-10-931-886-376
661	1806	100.0	344	5	US-10-805-667-523
662	1806	100.0	344	5	US-10-897-359-523
664	1806	100.0	344	5	US-10-893-802-523
665	1806	100.0	344	5	US-10-897-360-523
666	1806	100.0	344	5	US-10-955-952-376
669	1806	100.0	344	5	US-10-973-115B-376
678	1806	100.0	344	6	US-11-129-762-523
679	1806	100.0	344	6	US-11-290-153-376
680	1799	99.6	344	3	US-09-966-546-4
681	1799	99.6	344	3	US-09-966-546-6
682	1799	99.6	344	3	US-09-966-545-4
683	1799	99.6	344	3	US-09-966-545-6
684	1799	99.6	344	3	US-09-965-212-4
685	1799	99.6	344	3	US-09-965-212-6
686	1799	99.6	344	4	US-10-189-940-4
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689	1799	99.6	344	5	US-10-971-479-6
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691	1655.5	92.2	344	4	US-10-295-027-456
692	1650	91.4	355	4	US-10-306-133-1
693	1642	90.9	313	4	US-10-657-103-4
694	1639.5	90.8	344	4	US-10-306-133-3
695	1427.5	79.0	344	4	US-10-015-115-87
696	1295	71.7	250	4	US-10-311-823-15
697	1285.5	71.2	338	4	US-10-015-115-86
698	1268	70.2	345	4	US-10-161-572-59
699	1268	70.2	345	4	US-10-015-115-84
700	1268	70.2	345	5	US-10-696-639-46
701	1266	70.1	345	4	US-10-015-115-83
702	1259	69.7	345	4	US-10-015-115-85
703	938.5	52.0	338	4	US-10-038-854-159
704	931.5	51.6	338	3	US-09-808-602-69
705	931.5	51.6	338	3	US-09-800-198-58
706	931.5	51.6	338	4	US-10-161-572-58
707	931.5	51.6	338	4	US-10-038-854-158
708	931.5	51.6	338	4	US-10-042-865-52
709	930.5	51.5	350	3	US-09-808-602-71
710	930.5	51.5	350	3	US-09-800-198-60
711	926.5	51.3	338	3	US-09-808-602-72
712	926.5	51.3	338	3	US-09-800-198-61
713	926.5	51.3	338	4	US-10-042-865-91
714	893	49.4	383	3	US-09-978-418-38
715	893	49.4	383	5	US-10-485-231-38
716	873.5	48.4	203	4	US-10-187-975-108
717	852.5	47.2	326	4	US-10-106-698-5794
718	842	46.6	352	4	US-10-038-854-156
719	842	46.6	352	4	US-10-042-865-89
726	823	45.6	354	4	US-10-066-269-130
774	823	45.6	354	4	US-10-219-065-2
830	823	45.6	354	4	US-10-038-854-24
833	823	45.6	354	4	US-10-312-352-15
841	822	45.5	354	4	US-10-042-865-14
842	820	45.4	354	4	US-10-104-047-2965
843	820	45.4	354	6	US-11-072-512-2965
844	819	45.3	354	4	US-10-038-854-26
845	815	45.1	348	4	US-10-161-572-56
846	815	45.1	348	4	US-10-161-572-57
847	815	45.1	348	4	US-10-038-854-155
848	815	45.1	348	4	US-10-042-865-88
849	815	45.1	352	4	US-10-167-749-612
850	815	45.1	352	4	US-10-170-481A-612
851	815	45.1	352	4	US-10-210-028-612
852	815	45.1	352	4	US-10-162-521A-612
853	815	45.1	352	5	US-10-918-851-612
854	815	45.1	352	5	US-10-805-667-612
855	815	45.1	352	5	US-10-897-359-612
856	815	45.1	352	5	US-10-893-802-612
857	815	45.1	352	5	US-10-897-360-612
858	815	45.1	352	6	US-11-129-762-612
859	815	45.1	352	6	US-10-471-449-9
860	763	42.2	336	4	US-10-480-172-8
861	763	42.2	336	5	US-10-453-372-308
862	763	42.2	336	5	US-10-453-372-310
863	763	42.2	336	5	US-10-453-372-314
864	763	42.2	336	5	US-10-453-372-284
865	763	42.2	336	5	US-10-453-372-286
866	761	42.1	307	5	US-10-453-372-298
867	761	42.1	309	5	US-10-453-372-302
868	761	42.1	309	5	US-10-453-372-306
869	761	42.1	315	5	US-10-453-372-290

957	761	42.1	319	4	US-10-015-115-22	Sequence 22, Appl	1030	268.5	14.9	1496	4	US-10-021-660-125	Sequence 125, App
958	761	42.1	319	4	US-10-015-115-24	Sequence 24, Appl	1031	268.5	14.9	1496	4	US-10-331-496A-28	Sequence 28, Appl
959	761	42.1	319	5	US-10-453-372-292	Sequence 292, Appl	1032	268.5	14.9	1496	4	US-10-211-462-87	Sequence 87, Appl
960	761	42.1	319	5	US-10-453-372-296	Sequence 296, Appl	1033	268.5	14.9	1496	5	US-10-723-860-1721	Sequence 1721, Ap
961	761	42.1	320	5	US-10-453-372-312	Sequence 312, Appl	1034	268.5	14.9	1496	5	US-10-496-905-616	Sequence 616, App
962	761	42.1	325	5	US-10-453-372-324	Sequence 294, Appl	1035	268.5	14.9	1496	5	US-10-745-237-344	Sequence 344, App
963	760	42.1	336	5	US-10-453-372-282	Sequence 282, Appl	1036	268.5	14.9	1496	5	US-10-745-237-350	Sequence 350, App
964	760	42.1	336	5	US-10-453-372-318	Sequence 318, Appl	1037	268.5	14.9	1498	4	US-10-243-552-899	Sequence 899, App
965	757	41.9	307	4	US-10-015-115-26	Sequence 26, Appl	1038	268.5	14.9	1498	4	US-10-276-774-1957	Sequence 1957, Ap
966	757	41.9	319	5	US-10-453-372-300	Sequence 300, Appl	1039	266	14.7	36946	5	US-10-840-512-135	Sequence 155, App
967	757	41.9	336	5	US-10-453-372-316	Sequence 316, Appl	1040	261	14.5	1395	5	US-09-808-602-67	Sequence 67, App
968	726	40.2	336	4	US-10-332-947-53	Sequence 53, Appl	1041	261	14.5	1395	3	US-09-800-198-56	Sequence 56, Appl
969	721	39.9	336	4	US-10-015-115-28	Sequence 28, Appl	1042	261	14.5	1395	4	US-10-289-776-15	Sequence 15, Appl
970	721	39.9	336	5	US-10-453-372-304	Sequence 304, Appl	1043	261	14.5	1395	5	US-10-826-812-2	Sequence 2, Appl
971	720.5	39.9	281	3	US-09-764-853-561	Sequence 561, Appl	1044	261	14.5	1395	6	US-11-022-546-15	Sequence 15, Appl
972	687.5	38.1	253	5	US-10-453-372-288	Sequence 288, Appl	1045	260.5	14.4	496	6	US-11-097-143-12948	Sequence 12948, A
973	681.5	37.7	351	4	US-10-332-947-52	Sequence 52, Appl	1046	260	14.4	1395	6	US-11-097-143-31563	Sequence 31563, A
974	632	35.0	133	4	US-10-378-029-73	Sequence 73, Appl	1047	259	14.3	34350	5	US-10-745-237-394	Sequence 394, App
975	603	33.4	141	5	US-10-450-763-44207	Sequence 44207, A	1048	255.5	14.1	1024	5	US-10-737-318-44	Sequence 44, Appl
976	599	33.2	261	4	US-10-038-854-157	Sequence 157, Appl	1049	255.5	14.1	1024	5	US-10-737-318-46	Sequence 46, Appl
977	599	33.2	261	4	US-10-042-865-90	Sequence 90, Appl	1050	255	14.1	359	6	US-11-097-143-18552	Sequence 18552, A
978	569.5	31.5	130	5	US-10-450-763-44206	Sequence 44206, A	1051	254.5	14.1	5175	4	US-10-120-801-74	Sequence 74, Appl
979	527	29.2	256	4	US-10-480-172-14	Sequence 14, Appl	1052	254.5	14.1	5175	4	US-10-369-493-6859	Sequence 6859, Ap
980	525.5	29.1	872	5	US-10-450-763-44175	Sequence 44175, A	1053	254.5	14.1	5175	4	US-10-369-493-6861	Sequence 6861, Ap
981	472	26.1	241	4	US-10-480-172-12	Sequence 12, Appl	1054	254.5	14.1	5198	4	US-10-120-801-75	Sequence 75, Appl
982	338.5	18.7	413	6	US-11-097-143-35247	Sequence 35247, A	1055	254.5	14.1	5198	4	US-10-369-493-6858	Sequence 6858, Ap
983	333	18.4	315	6	US-11-097-143-23718	Sequence 23718, A	1056	254.5	14.1	5198	4	US-10-369-493-6860	Sequence 6860, Ap
984	308.5	17.1	528	4	US-10-108-605-49	Sequence 49, Appl	1057	254.5	14.1	5198	4	US-10-346-863-34	Sequence 34, Appl
985	306	16.9	545	6	US-11-097-143-14514	Sequence 14514, A	1058	253.5	14.0	404	3	US-09-977-418-24	Sequence 24, Appl
986	297.5	16.5	333	6	US-11-097-143-3633	Sequence 3633, Ap	1059	253.5	14.0	404	3	US-09-977-033A-24	Sequence 24, Appl
987	290.5	16.1	2572	4	US-10-114-153-86	Sequence 86, Appl	1060	253.5	14.0	404	3	US-09-977-751C-24	Sequence 24, Appl
988	290.5	16.1	2673	4	US-10-120-801-76	Sequence 76, Appl	1061	253.5	14.0	404	3	US-09-977-639A-24	Sequence 24, Appl
989	290.5	16.1	2673	5	US-10-934-998-101	Sequence 101, Appl	1062	253.5	14.0	404	3	US-09-977-819B-24	Sequence 24, Appl
990	290.5	16.1	4495	4	US-10-138-588-20	Sequence 20, Appl	1063	253.5	14.0	404	4	US-10-161-572-44	Sequence 44, Appl
991	290.5	16.1	4495	5	US-10-453-372-1002	Sequence 1002, Ap	1064	253	14.0	570	4	US-10-311-823-13	Sequence 13, Appl
992	290.5	16.1	4995	4	US-10-032-189-128	Sequence 128, App	1065	253	14.0	586	6	US-11-097-143-11298	Sequence 11298, A
993	290.5	16.1	5636	4	US-10-120-801-72	Sequence 72, Appl	1066	250.5	13.9	885	6	US-11-097-143-11298	Sequence 11298, A
994	290.5	16.1	5636	4	US-10-023-634-93	Sequence 93, Appl	1067	250	13.8	374	4	US-10-311-823-16	Sequence 16, Appl
995	290.5	16.1	5636	4	US-10-408-765A-1895	Sequence 895, Ap	1068	250	13.8	442	4	US-10-311-823-12	Sequence 12, Appl
996	290.5	16.1	5636	5	US-10-934-998-81	Sequence 81, Appl	1069	250	13.8	458	4	US-10-311-823-4	Sequence 4, Appl
997	288.5	16.0	707	4	US-10-138-588-18	Sequence 18, Appl	1070	250	13.8	1219	5	US-10-450-763-42459	Sequence 42459, A
998	288.5	16.0	707	5	US-10-453-372-998	Sequence 998, App	1071	250	13.8	1219	5	US-10-094-886-52	Sequence 52, Appl
999	288.5	16.0	712	5	US-10-453-372-1000	Sequence 1000, Ap	1072	250	13.8	1315	5	US-10-453-372-1034	Sequence 1034, Ap
1000	288.5	16.0	961	4	US-10-162-325-42	Sequence 42, Appl	1073	250	13.8	1335	4	US-10-453-372-1030	Sequence 1030, Ap
1001	288.5	16.0	961	6	US-11-051-724-42	Sequence 42, Appl	1074	250	13.8	1386	4	US-10-094-886-38	Sequence 38, Appl
1002	288.5	16.0	1240	5	US-10-019-763-34292	Sequence 34292, A	1075	249.5	13.8	607	3	US-09-991-326-12	Sequence 12, Appl
1003	288.5	16.0	1336	4	US-10-019-065A-33	Sequence 33, Appl	1076	249.5	13.8	1040	4	US-10-712-124-10	Sequence 10, Appl
1004	288.5	16.0	1902	4	US-10-114-153-88	Sequence 88, Appl	1077	248	13.7	467	6	US-11-097-143-33438	Sequence 33438, A
1005	288.5	16.0	1902	5	US-10-453-372-1004	Sequence 1004, Ap	1078	246.5	13.6	1007	5	US-10-408-765A-118	Sequence 118, App
1006	288.5	16.0	1953	4	US-10-115-479-88	Sequence 88, Appl	1079	246.5	13.6	1007	5	US-10-329-258-23	Sequence 23, Appl
1007	288.5	16.0	3645	4	US-10-032-189-127	Sequence 127, App	1080	246.5	13.6	1018	4	US-10-367-978-67	Sequence 67, Appl
1008	288.5	16.0	3645	4	US-10-120-801-73	Sequence 73, Appl	1081	246.5	13.6	1018	4	US-10-712-124-88	Sequence 88, Appl
1009	288.5	16.0	4126	6	US-11-049-637-4	Sequence 4, Appl	1082	246.5	13.6	1018	5	US-10-631-467-948	Sequence 948, App
1010	288.5	16.0	5518	6	US-11-049-637-2	Sequence 2, Appl	1083	244.5	13.5	512	4	US-10-094-749-2493	Sequence 2493, Ap
1011	288.5	16.0	5622	5	US-10-773-446-128	Sequence 128, App	1084	243.5	13.5	605	3	US-09-991-326-8	Sequence 8, Appl
1012	288.5	16.0	5635	5	US-10-451-168-78	Sequence 78, Appl	1085	242.5	13.4	792	5	US-10-450-763-33418	Sequence 33418, A
1013	288.5	16.0	5635	5	US-10-980-387-78	Sequence 78, Appl	1086	242.5	13.4	893	5	US-10-450-763-30617	Sequence 30617, A
1014	288.5	16.0	5636	6	US-11-065-695-20	Sequence 20, Appl	1087	242.5	13.4	893	5	US-10-450-763-30970	Sequence 30970, A
1015	284.5	15.8	467	6	US-11-097-143-15924	Sequence 15924, A	1088	242	13.4	2586	3	US-09-729-485A-11	Sequence 11, Appl
1016	278.5	15.4	4162	4	US-10-023-634-92	Sequence 92, Appl	1089	242	13.4	2586	3	US-09-729-485A-14	Sequence 14, Appl
1017	276	15.3	733	4	US-10-094-749-3192	Sequence 3192, Ap	1090	242	13.4	2586	3	US-09-802-318-11	Sequence 11, Appl
1018	276	15.3	848	4	US-10-311-509-21	Sequence 21, Appl	1091	242	13.4	2586	3	US-09-802-318-14	Sequence 14, Appl
1019	276	15.3	848	5	US-10-482-029-204	Sequence 204, Appl	1092	242	13.4	2586	3	US-09-905-129-11	Sequence 11, Appl
1020	276	15.3	848	5	US-10-852-335A-113	Sequence 113, App	1093	242	13.4	2586	3	US-09-905-129-14	Sequence 14, Appl
1021	276	15.3	848	5	US-10-992-287-48	Sequence 48, Appl	1094	242	13.4	2586	3	US-09-991-630-11	Sequence 11, Appl
1022	275.5	15.3	853	5	US-10-496-905-513	Sequence 513, App	1095	242	13.4	2586	3	US-09-991-630-14	Sequence 14, Appl
1023	275	15.2	848	4	US-10-207-655-180	Sequence 180, App	1096	242	13.4	2586	4	US-10-454-351-11	Sequence 11, Appl
1024	274	15.2	1477	4	US-10-274-583-20	Sequence 20, Appl	1097	242	13.4	2586	4	US-10-454-351-14	Sequence 14, Appl
1025	273.5	15.1	1356	4	US-10-085-198-108	Sequence 108, App	1098	242	13.4	2587	3	US-09-729-485A-16	Sequence 16, Appl
1026	271.5	15.0	1426	4	US-10-085-198-106	Sequence 106, App	1099	242	13.4	2587	3	US-09-802-318-16	Sequence 16, Appl
1027	270	15.0	729	6	US-11-097-143-32490	Sequence 32490, A	1100	242	13.4	2587	3	US-09-905-129-16	Sequence 16, Appl
1028	269	14.9	152	4	US-10-091-438-168	Sequence 168, App	1101	242	13.4	2587	3	US-09-991-630-16	Sequence 16, Appl
1029	268.5	14.9	1479	4	US-10-231-956A-325	Sequence 325, App	1102	242	13.4	2587	4	US-10-454-351-16	Sequence 16, Appl

1103	242	13.4	2589	3	US-09-991-630-24	Sequence 24, Appl	1176	239.5	12.7	1224	4	US-10-435-751-185	Sequence 185, App
1104	242	13.4	2589	4	US-10-454-351-24	Sequence 24, Appl	1177	239.5	12.7	1224	4	US-10-435-751-191	Sequence 191, App
1105	241.5	13.4	2589	5	US-10-631-467-1637	Sequence 1637, Ap	1178	239.5	12.7	1224	4	US-10-435-751-196	Sequence 196, App
1106	241	13.3	891	5	US-10-450-763-37895	Sequence 37895, A	1179	239.5	12.7	1224	4	US-10-435-751-197	Sequence 197, App
1107	240	13.3	3707	5	US-10-852-335A-139	Sequence 139, App	1180	239.5	12.7	1224	4	US-10-435-751-198	Sequence 198, App
1108	238.5	13.2	1024	5	US-10-737-318-41	Sequence 41, Appl	1181	239.5	12.7	1224	4	US-10-435-751-199	Sequence 199, App
1109	235.5	13.0	967	5	US-10-453-712-714	Sequence 714, App	1182	239.5	12.7	1224	4	US-10-435-751-208	Sequence 208, App
1110	235.5	13.0	2623	4	US-10-454-351-32	Sequence 32, Appl	1183	239.5	12.7	1224	4	US-10-408-765A-1408	Sequence 1408, Ap
1111	235	13.0	662	4	US-10-369-493-6726	Sequence 6726, Ap	1184	229	12.7	1056	4	US-10-098-871-65	Sequence 65, Appl
1112	232.5	12.9	967	5	US-10-453-372-712	Sequence 712, App	1185	229	12.7	3588	4	US-10-741-601-378	Sequence 378, App
1113	232.5	12.9	2783	4	US-10-368-493-6344	Sequence 6344, Ap	1186	229	12.7	3588	5	US-10-741-600-1104	Sequence 1104, Ap
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1115	232	12.8	2591	5	US-10-453-372-718	Sequence 718, App	1188	229	12.7	4346	4	US-10-741-601-377	Sequence 377, App
1116	232	12.8	2617	5	US-10-453-372-716	Sequence 716, App	1189	229	12.7	4346	5	US-10-741-600-1103	Sequence 1103, Ap
1117	232	12.8	2617	4	US-10-032-189-46	Sequence 46, Appl	1190	229	12.7	4346	5	US-10-995-561-671	Sequence 671, App
1118	232	12.8	2617	5	US-10-453-372-666	Sequence 666, App	1191	229	12.7	4347	4	US-10-741-601-376	Sequence 376, App
1119	232	12.8	2617	5	US-10-453-372-732	Sequence 732, App	1192	229	12.7	4347	5	US-10-741-600-1102	Sequence 1102, Ap
1120	232	12.8	2617	5	US-10-453-372-734	Sequence 734, App	1193	229	12.7	4347	5	US-10-995-561-670	Sequence 670, App
1121	232	12.8	2617	5	US-10-453-372-736	Sequence 736, App	1194	229	12.7	4370	4	US-10-408-765A-1267	Sequence 1267, Ap
1122	232	12.8	2617	5	US-10-453-372-738	Sequence 738, App	1195	229	12.7	4390	6	US-11-169-041-169	Sequence 169, App
1123	232	12.8	2617	5	US-10-453-372-740	Sequence 740, App	1196	228	12.6	1483	5	US-10-450-763-46695	Sequence 46695, A
1124	232	12.8	2617	5	US-10-453-372-742	Sequence 742, App	1197	227.5	12.6	8523	5	US-10-840-512-162	Sequence 162, App
1125	232	12.8	2617	5	US-10-453-372-744	Sequence 744, App	1198	227	12.6	1189	6	US-11-050-857-953	Sequence 953, App
1126	232	12.8	2617	5	US-10-453-372-746	Sequence 746, App	1199	227	12.6	1189	6	US-11-051-720-1694	Sequence 1694, Ap
1127	232	12.8	2617	5	US-10-453-372-748	Sequence 748, App	1200	226	12.5	717	6	US-11-050-857-954	Sequence 954, App
1128	232	12.8	2617	5	US-10-453-372-750	Sequence 750, App	1201	226	12.5	717	6	US-11-051-720-1695	Sequence 1695, Ap
1129	232	12.8	3931	4	US-10-120-801-18	Sequence 18, Appl	1202	226	12.5	6642	4	US-10-369-493-5013	Sequence 5013, Ap
1130	230.5	12.8	860	6	US-11-172-410-2	Sequence 2, Appl	1203	225.5	12.5	869	4	US-10-471-115-18	Sequence 18, Appl
1131	230.5	12.8	868	4	US-10-016-283-1	Sequence 1, Appl	1204	225	12.5	4391	5	US-10-478-451-1	Sequence 1, Appl
1132	230.5	12.8	961	5	US-10-453-372-726	Sequence 726, App	1205	224.5	12.4	477	4	US-10-613-413A-23	Sequence 23, Appl
1133	230.5	12.8	961	5	US-10-453-372-728	Sequence 728, App	1206	224.5	12.4	477	5	US-10-885-225-23	Sequence 23, Appl
1134	230	12.7	4393	4	US-10-231-956A-366	Sequence 366, App	1207	224.5	12.4	477	5	US-10-954-094-23	Sequence 23, Appl
1135	230	12.7	4393	5	US-10-741-600-1105	Sequence 1105, Ap	1208	224.5	12.4	869	3	US-09-817-487A-2	Sequence 2, Appl
1136	230	12.7	4419	5	US-10-821-234-1155	Sequence 1155, Ap	1209	224.5	12.4	981	5	US-10-450-763-52992	Sequence 52992, A
1137	230	12.7	4436	5	US-10-450-763-53624	Sequence 53624, A	1210	224.5	12.4	1171	4	US-10-435-751-5	Sequence 5, Appl
1138	229.5	12.7	849	4	US-10-435-751-161	Sequence 161, App	1211	224.5	12.4	1171	4	US-10-435-751-21	Sequence 21, Appl
1139	229.5	12.7	851	4	US-10-435-751-162	Sequence 162, App	1212	224.5	12.4	1171	4	US-10-435-751-154	Sequence 154, App
1140	229.5	12.7	869	4	US-10-016-283-33	Sequence 33, Appl	1213	224.5	12.4	1171	4	US-10-435-751-156	Sequence 156, App
1141	229.5	12.7	869	5	US-10-745-237-274	Sequence 274, App	1214	224.5	12.4	1171	4	US-10-435-751-200	Sequence 200, App
1142	229.5	12.7	893	4	US-10-435-751-7	Sequence 7, Appl	1215	224.5	12.4	1224	4	US-10-435-751-30	Sequence 30, Appl
1143	229.5	12.7	893	4	US-10-435-751-22	Sequence 22, Appl	1216	224.5	12.4	1224	5	US-10-723-860-2585	Sequence 2585, Ap
1144	229.5	12.7	893	4	US-10-435-751-160	Sequence 160, App	1217	224.5	12.4	1224	5	US-10-756-149-5414	Sequence 5414, Ap
1145	229.5	12.7	893	4	US-10-435-751-201	Sequence 201, App	1218	224.5	12.4	1224	5	US-10-631-467-771	Sequence 771, App
1146	229.5	12.7	1117	4	US-10-435-751-9	Sequence 9, Appl	1219	224.5	12.4	1645	5	US-10-450-763-50367	Sequence 50367, A
1147	229.5	12.7	1117	4	US-10-435-751-23	Sequence 23, Appl	1220	224.5	12.4	1765	5	US-10-450-763-52990	Sequence 52990, A
1148	229.5	12.7	1117	4	US-10-435-751-166	Sequence 166, App	1221	224.5	12.4	1944	5	US-10-450-763-42376	Sequence 42376, A
1149	229.5	12.7	1117	4	US-10-435-751-168	Sequence 168, App	1222	224	12.4	434	5	US-10-450-763-32378	Sequence 32378, A
1150	229.5	12.7	1117	4	US-10-435-751-202	Sequence 202, App	1223	224	12.4	737	5	US-10-450-763-32378	Sequence 32378, A
1151	229.5	12.7	1183	4	US-10-435-751-13	Sequence 13, Appl	1226	224	12.4	1059	3	US-09-905-291A-290	Sequence 290, App
1152	229.5	12.7	1183	4	US-10-435-751-25	Sequence 25, Appl	1294	224	12.4	1059	4	US-10-299-976-290	Sequence 290, App
1153	229.5	12.7	1183	4	US-10-435-751-178	Sequence 178, App	1295	224	12.4	1059	4	US-10-299-937-290	Sequence 290, App
1154	229.5	12.7	1183	4	US-10-435-751-180	Sequence 180, App	1296	224	12.4	1059	4	US-10-298-993-290	Sequence 290, App
1155	229.5	12.7	1183	4	US-10-435-751-204	Sequence 204, App	1297	224	12.4	1059	4	US-10-448-923-290	Sequence 290, App
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SUMMARIES

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5	229.5	12.7	869	7	US-11-365-989-216
6	229	12.7	4391	7	US-11-183-325-56
7	224.5	12.4	477	7	US-11-154-977-23
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100	164	9.1	439	7	US-11-154-977-7	Sequence 7, Appl
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109	162	9-0	654	6	US-10-669-920-433	Sequence 433, App	182	141	7.8	448	6	US-10-669-920-577	Sequence 577, App
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115	157.5	8-7	697	7	US-11-246-999-149	Sequence 149, App	188	140.5	7.8	1083	6	US-10-669-920-1435	Sequence 1435, Ap
116	157	8-7	335	6	US-10-523-634-330	Sequence 330, App	189	140.5	7.8	1089	7	US-11-248-956-22	Sequence 22, Appl
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118	157	8-7	734	7	US-11-315-529-8	Sequence 8, Appl	191	140	7.8	890	6	US-10-553-520-180	Sequence 180, App
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137	150.5	8-3	449	6	US-10-669-920-573	Sequence 573, App	210	136	7.5	303	7	US-11-293-697-2977	Sequence 2977, Ap
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140	150.5	8-3	449	6	US-10-669-920-627	Sequence 627, App	213	134.5	7.4	387	7	US-11-378-707-2	Sequence 2, Appl
141	150.5	8-3	1298	6	US-10-505-928-274	Sequence 274, App	214	134.5	7.4	534	7	US-11-355-735-7	Sequence 7, Appl
142	150.5	8-3	1298	7	US-11-248-356-12	Sequence 12, Appl	215	134.5	7.4	534	7	US-11-378-707-11	Sequence 11, Appl
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145	150.5	8-3	1363	7	US-11-365-989-146	Sequence 146, App	218	134.5	7.4	698	7	US-11-355-735-9	Sequence 9, Appl
146	149.5	8-3	349	7	US-11-105-233-201	Sequence 201, App	219	134.5	7.4	698	7	US-11-346-468-9	Sequence 9, Appl
147	149.5	8-3	364	7	US-11-090-997-366	Sequence 366, App	220	134.5	7.4	707	7	US-11-365-989-136	Sequence 136, App
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149	149	8-3	373	7	US-11-287-573-26	Sequence 26, Appl	222	134.5	7.4	1235	6	US-10-530-187-243	Sequence 243, App
150	147	8-1	394	6	US-10-538-066-754	Sequence 754, App	223	134	7.4	435	6	US-11-346-008-24	Sequence 24, Appl
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152	146	8-1	1083	6	US-10-519-342-5	Sequence 5, Appl	225	133.5	7.4	697	6	US-10-669-920-593	Sequence 593, App
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156	145.5	8-1	1012	6	US-10-519-342-3	Sequence 3, Appl	229	133	7.4	839	7	US-11-326-389-14	Sequence 14, Appl
157	145	8-0	776	6	US-10-669-920-184	Sequence 184, App	230	132.5	7.3	534	7	US-11-378-707-13	Sequence 13, Appl
158	145	8-0	972	7	US-11-255-147-8	Sequence 8, Appl	231	132.5	7.3	534	7	US-11-378-707-18	Sequence 18, Appl
159	145	8-0	972	7	US-11-248-956-5	Sequence 5, Appl	232	132	7.3	1518	6	US-10-669-920-758	Sequence 758, App
160	145	8-0	972	7	US-11-365-989-126	Sequence 126, App	233	131.5	7.3	434	6	US-11-154-977-85	Sequence 85, Appl
161	144	8-0	382	6	US-10-669-920-575	Sequence 575, App	234	131	7.3	1106	6	US-10-570-909-78	Sequence 78, Appl
162	144	8-0	382	6	US-10-669-920-597	Sequence 597, App	235	131	7.3	1106	7	US-11-248-956-23	Sequence 23, Appl
163	144	8-0	393	6	US-11-315-529-12	Sequence 12, Appl	236	131	7.3	1106	7	US-11-365-989-132	Sequence 132, App
164	144	8-0	407	7	US-11-154-977-95	Sequence 95, Appl	237	130.5	7.2	443	6	US-10-669-920-1164	Sequence 1164, Ap
165	144	8-0	891	7	US-11-358-419-25	Sequence 25, Appl	238	130	7.2	394	7	US-11-265-762-78	Sequence 78, Appl
166	143	7-9	416	7	US-11-293-697-4389	Sequence 4389, Ap	239	130	7.2	798	6	US-10-669-920-193	Sequence 193, App
167	143	7-9	441	7	US-11-090-997-548	Sequence 548, App	240	130	7.2	798	6	US-10-669-920-195	Sequence 195, App
168	143	7-9	687	6	US-10-508-580-9	Sequence 9, Appl	241	130	7.2	798	6	US-10-669-920-205	Sequence 205, App
169	143	7-9	688	6	US-11-300-928-47	Sequence 47, Appl	242	129	7.1	802	7	US-11-248-956-9	Sequence 9, Appl
170	143	7-9	688	6	US-10-508-580-10	Sequence 10, Appl	243	129	7.1	417	6	US-10-505-928-664	Sequence 664, App
171	142.5	7-9	735	7	US-11-170-797-6	Sequence 6, Appl	244	129	7.1	480	7	US-11-346-468-135	Sequence 135, App
172	142	7-9	351	6	US-10-523-834-331	Sequence 331, App	245	128.5	7.1	477	6	US-10-527-101-22	Sequence 22, Appl
173	142	7-9	794	6	US-10-669-920-186	Sequence 186, App	246	128	7.1	370	7	US-11-265-762-76	Sequence 76, Appl
174	141.5	7-8	431	7	US-11-409-216-2	Sequence 2, Appl	247	128	7.1	372	7	US-11-251-465-7	Sequence 71, Appl
175	141.5	7-8	469	6	US-10-519-342-6	Sequence 6, Appl	248	128	7.1	806	7	US-11-251-465-22	Sequence 22, Appl
176	141.5	7-8	480	7	US-11-265-762-158	Sequence 158, App	249	128	7.1	806	7	US-11-365-989-138	Sequence 138, App
177	141.5	7-8	791	7	US-11-090-997-1580	Sequence 1580, Ap	250	127.5	7.1	339	6	US-10-669-920-424	Sequence 424, App

251	127	7.0	271	6	US-10-669-920-581	Sequence 581, App	325	116.5	6.5	615	7	US-11-090-997-796	Sequence 796, App
252	127	7.0	271	6	US-10-669-920-633	Sequence 633, App	326	116	6.4	377	7	US-11-241-836-8	Sequence 8, Appli
253	127	7.0	720	6	US-10-669-920-595	Sequence 595, App	327	116	6.4	410	7	US-11-090-997-1400	Sequence 1400, Ap
254	127	7.0	720	6	US-10-669-920-617	Sequence 617, App	328	116	6.4	451	7	US-11-355-735-17	Sequence 17, Appl
255	127	7.0	720	6	US-10-669-920-631	Sequence 631, App	329	116	6.4	451	7	US-11-346-468-17	Sequence 17, Appl
256	127	7.0	917	7	US-11-332-434-24	Sequence 24, Appl	330	116	6.4	1463	7	US-11-090-997-360	Sequence 360, App
257	127	7.0	917	7	US-11-332-434-26	Sequence 26, Appl	331	115.5	6.4	232	7	US-11-346-008-23	Sequence 23, Appl
258	127	7.0	996	6	US-10-669-920-69	Sequence 69, Appl	332	115.5	6.4	526	7	US-11-246-999-121	Sequence 121, App
259	126.5	7.0	365	6	US-10-505-928-148	Sequence 148, App	333	115.5	6.4	798	6	US-10-669-920-199	Sequence 199, App
260	126	7.0	477	7	US-11-326-389-4	Sequence 4, Appli	334	115	6.4	385	7	US-11-241-836-4	Sequence 4, Appli
261	126	7.0	537	7	US-11-326-389-6	Sequence 6, Appli	335	114.5	6.3	144	7	US-11-154-977-129	Sequence 129, App
262	126	7.0	553	7	US-11-326-389-8	Sequence 8, Appli	336	114.5	6.3	235	7	US-11-346-008-25	Sequence 25, Appl
263	126	7.0	822	7	US-11-326-389-2	Sequence 2, Appli	337	114.5	6.3	466	7	US-11-211-917-30	Sequence 30, Appl
264	126	7.0	822	7	US-11-365-989-176	Sequence 176, App	338	114	6.3	300	6	US-10-669-920-441	Sequence 441, App
265	126	6.9	262	7	US-11-154-977-53	Sequence 53, Appl	339	114	6.3	302	6	US-10-553-520-93	Sequence 93, Appl
266	125	6.9	370	7	US-11-241-836-10	Sequence 10, Appl	340	113.5	6.3	117	7	US-11-154-977-139	Sequence 139, App
267	124	6.9	993	6	US-10-511-937-2463	Sequence 2463, Ap	341	113.5	6.3	286	6	US-10-669-920-197	Sequence 197, App
268	124	6.9	993	7	US-11-365-989-124	Sequence 124, App	342	113.5	6.3	307	6	US-10-669-920-191	Sequence 191, App
269	124	6.9	999	6	US-10-519-083-4	Sequence 4, Appli	343	113.5	6.3	374	6	US-10-511-937-2420	Sequence 2420, Ap
270	124	6.9	999	7	US-11-365-989-184	Sequence 184, App	344	113.5	6.3	374	6	US-11-363-149-67	Sequence 67, Appl
271	124	6.8	645	7	US-11-354-079-3	Sequence 3, Appli	345	113.5	6.3	374	7	US-11-363-151-67	Sequence 67, Appl
272	123.5	6.8	645	7	US-11-406-679-4	Sequence 4, Appli	346	113.5	6.3	547	6	US-10-511-937-2969	Sequence 2969, Ap
273	123.5	6.8	645	7	US-11-347-808-93	Sequence 93, Appl	347	113.5	6.3	686	6	US-10-669-920-189	Sequence 189, App
274	123.5	6.8	386	7	US-11-241-836-6	Sequence 6, Appli	348	113.5	6.3	686	6	US-10-669-920-201	Sequence 201, App
275	123	6.8	476	7	US-11-326-389-12	Sequence 12, Appl	349	113.5	6.3	686	6	US-10-669-920-203	Sequence 203, App
276	123	6.8	821	7	US-11-326-389-10	Sequence 10, Appl	350	113.5	6.3	1465	7	US-11-090-997-1322	Sequence 1322, Ap
277	123	6.8	320	7	US-11-154-977-97	Sequence 97, Appl	351	113	6.3	410	7	US-11-293-697-3741	Sequence 3741, Ap
278	122.5	6.8	669	7	US-11-223-400-11	Sequence 11, Appl	352	113	6.3	458	7	US-11-346-008-8	Sequence 8, Appli
279	122.5	6.8	258	7	US-11-154-977-117	Sequence 117, App	353	113	6.3	458	7	US-11-350-145-2	Sequence 2, Appli
280	122	6.8	382	7	US-11-241-836-2	Sequence 2, Appli	354	113	6.3	458	7	US-11-373-358-2	Sequence 2, Appli
281	122	6.8	1016	6	US-10-519-083-2	Sequence 2, Appli	355	113	6.3	458	7	US-11-387-256-2	Sequence 2, Appli
282	122	6.8	915	7	US-11-332-434-22	Sequence 22, Appl	356	113	6.3	467	7	US-11-246-999-34	Sequence 34, Appl
283	122	6.8	293	7	US-11-154-977-107	Sequence 107, App	357	112.5	6.2	406	7	US-11-293-697-4513	Sequence 4513, Ap
284	121.5	6.7	390	7	US-11-353-554-2	Sequence 2, Appli	358	112.5	6.2	570	1	US-09-784-950-18	Sequence 18, Appl
285	121.5	6.7	631	7	US-11-241-836-15	Sequence 15, Appl	359	112.5	6.2	669	6	US-10-549-460-4	Sequence 4, Appli
286	121.5	6.7	723	6	US-10-669-920-439	Sequence 439, App	360	112.5	6.2	964	6	US-10-549-460-2	Sequence 2, Appli
287	121.5	6.7	340	7	US-11-180-855-3	Sequence 3, Appli	361	111.5	6.2	458	7	US-11-346-008-10	Sequence 10, Appl
288	121	6.7	463	7	US-11-378-707-20	Sequence 20, Appl	362	111.5	6.2	458	7	US-11-346-009-2	Sequence 2, Appli
289	121	6.7	900	7	US-11-332-434-10	Sequence 10, Appl	363	111.5	6.2	458	7	US-11-346-145-4	Sequence 4, Appli
290	121	6.7	900	7	US-11-346-007-2	Sequence 2, Appli	364	111.5	6.2	458	7	US-11-373-358-4	Sequence 4, Appli
291	121	6.7	902	7	US-11-332-434-12	Sequence 12, Appl	365	111.5	6.2	458	7	US-11-387-256-4	Sequence 4, Appli
292	121	6.7	902	7	US-11-332-434-14	Sequence 14, Appl	366	111.5	6.2	566	7	US-11-441-780-8	Sequence 8, Appli
293	121	6.7	902	7	US-11-332-434-12	Sequence 12, Appl	367	111	6.1	398	6	US-10-511-937-2405	Sequence 2405, Ap
294	120.5	6.7	295	7	US-11-154-977-33	Sequence 33, Appl	368	111	6.1	398	6	US-10-700-439-156	Sequence 156, App
295	120.5	6.7	915	7	US-11-332-434-16	Sequence 16, Appl	369	110.5	6.1	365	7	US-11-293-697-3883	Sequence 3883, Ap
296	120.5	6.7	917	7	US-11-332-434-18	Sequence 18, Appl	370	110.5	6.1	584	7	US-11-289-102-272	Sequence 272, App
297	120.5	6.7	917	7	US-11-332-434-20	Sequence 20, Appl	371	110.5	6.1	640	6	US-10-833-833-84	Sequence 84, Appl
298	120	6.6	934	7	US-11-247-437-10	Sequence 10, Appl	372	110.5	6.1	934	7	US-11-265-762-156	Sequence 156, App
299	120	6.6	934	7	US-11-033-476-5	Sequence 5, Appli	373	110.5	6.1	1215	6	US-10-505-928-75	Sequence 75, Appl
300	119.5	6.6	268	7	US-11-154-977-43	Sequence 43, Appl	374	110	6.1	432	7	US-11-293-697-3406	Sequence 3406, Ap
301	119.5	6.6	442	7	US-11-246-999-99	Sequence 99, Appl	375	110	6.1	771	7	US-11-191-244-68	Sequence 68, Appl
302	119.5	6.6	462	7	US-11-293-697-3457	Sequence 3457, Ap	376	109.5	6.1	443	6	US-10-981-300-20	Sequence 20, Appl
303	119	6.6	131	7	US-11-197-712-341	Sequence 341, App	377	109.5	6.1	450	6	US-10-669-920-1169	Sequence 1169, Ap
304	119	6.6	480	7	US-11-346-468-133	Sequence 133, App	378	109.5	6.1	451	6	US-10-669-920-1171	Sequence 1171, Ap
305	119	6.6	910	7	US-11-332-434-2	Sequence 2, Appli	379	109.5	6.1	470	7	US-11-167-767-32	Sequence 32, Appl
306	118.5	6.6	519	6	US-10-548-727-14	Sequence 14, Appl	380	109.5	6.1	473	6	US-10-669-920-1167	Sequence 1167, Ap
307	118.5	6.6	536	6	US-10-549-460-14	Sequence 14, Appl	381	109.5	6.1	470	6	US-10-505-928-499	Sequence 499, App
308	118.5	6.6	931	6	US-10-549-460-10	Sequence 10, Appl	382	109.5	6.1	532	6	US-10-505-928-499	Sequence 4, Appli
309	118.5	6.6	931	6	US-10-508-580-13	Sequence 13, Appl	383	109.5	6.1	566	6	US-10-833-833-79	Sequence 79, Appl
310	118.5	6.6	992	7	US-11-090-997-1340	Sequence 1340, Ap	384	109.5	6.1	566	6	US-10-833-833-81	Sequence 81, Appl
311	118.5	6.6	992	6	US-11-090-997-1344	Sequence 1344, Ap	385	109	6.0	429	7	US-11-315-529-4	Sequence 4, Appli
312	118	6.5	989	6	US-10-669-920-72	Sequence 72, Appl	386	108.5	6.0	148	7	US-11-154-977-65	Sequence 65, Appl
313	117.5	6.5	900	7	US-11-332-434-4	Sequence 4, Appli	387	108	6.0	269	7	US-11-412-325-78	Sequence 78, Appl
314	117.5	6.5	902	7	US-11-332-434-6	Sequence 6, Appli	388	108	6.0	319	6	US-10-511-937-2976	Sequence 2976, Ap
315	117.5	6.5	902	7	US-11-332-434-8	Sequence 8, Appli	389	107.5	6.0	121	7	US-11-154-977-75	Sequence 75, Appl
316	117	6.5	440	7	US-11-251-465-65	Sequence 65, Appl	390	107	5.9	316	7	US-11-355-735-11	Sequence 11, Appl
317	117	6.5	449	7	US-11-251-465-68	Sequence 68, Appl	391	107	5.9	316	7	US-11-346-468-11	Sequence 11, Appl
318	117	6.5	733	7	US-11-365-989-134	Sequence 134, App	392	106.5	5.9	336	7	US-11-441-780-6	Sequence 6, Appli
319	117	6.5	885	6	US-10-505-928-432	Sequence 432, App	393	106.5	5.9	719	7	US-11-293-697-3841	Sequence 3841, Ap
320	117	6.5	885	7	US-11-251-465-20	Sequence 20, Appl	394	106	5.9	347	7	US-11-073-360-184	Sequence 184, App
321	117	6.5	894	7	US-11-251-465-21	Sequence 21, Appl	395	105	5.8	269	1	US-09-784-950-14	Sequence 14, Appl
322	117	6.5	894	7	US-11-365-989-182	Sequence 182, App	396	104	5.8	384	7	US-11-293-697-2595	Sequence 2595, Ap
323	117	6.5	1618	7	US-11-375-615-46	Sequence 46, Appl	397	104	5.8	465	6	US-10-540-959-5	Sequence 5, Appli
324	116.5	6.5	315	7	US-11-305-843-12	Sequence 12, Appl							

398	103.5	5.7	455	7	US-11-346-008-13	Sequence 13, Appl	472	96	5.3	446	7	US-11-197-665-50	Sequence 50, Appl
399	103.5	5.7	538	7	US-11-246-999-138	Sequence 128, App	473	96	5.3	790	7	US-11-365-989-174	Sequence 174, App
400	103.5	5.7	943	7	US-11-370-424-7	Sequence 7, Appl	474	96	5.3	896	6	US-10-566-886-16	Sequence 16, Appl
401	103	5.7	247	7	US-11-287-573-48	Sequence 48, Appl	475	95.5	5.3	281	7	US-11-294-448-3	Sequence 3, Appl
402	103	5.7	943	7	US-11-365-989-210	Sequence 210, App	476	95.5	5.3	291	7	US-11-154-977-45	Sequence 45, Appl
403	103	5.7	1326	7	US-11-090-997-1476	Sequence 1476, App	477	95.5	5.3	318	7	US-11-154-977-35	Sequence 35, Appl
404	103	5.7	1346	7	US-11-090-997-1480	Sequence 1480, App	478	95.5	5.3	375	7	US-11-297-134-54	Sequence 54, Appl
405	102.5	5.7	172	7	US-11-305-447-13	Sequence 13, Appl	479	95.5	5.3	471	7	US-11-293-697-4285	Sequence 4285, App
406	102.5	5.7	197	7	US-11-305-447-11	Sequence 11, Appl	480	95.5	5.3	471	7	US-11-293-697-4294	Sequence 4294, App
407	102.5	5.7	232	7	US-11-305-447-6	Sequence 6, Appl	481	95	5.3	264	7	US-11-154-977-39	Sequence 39, Appl
408	102.5	5.7	257	7	US-11-305-447-2	Sequence 2, Appl	482	95	5.3	282	7	US-11-294-448-5	Sequence 5, Appl
409	102.5	5.7	357	6	US-10-540-959-2	Sequence 2, Appl	483	95	5.3	282	7	US-11-105-233-165	Sequence 165, App
410	102.5	5.7	518	6	US-10-560-299-4	Sequence 4, Appl	484	95	5.3	799	7	US-11-361-415-83	Sequence 83, Appl
411	102	5.6	269	6	US-10-669-920-263	Sequence 263, App	485	94.5	5.2	460	7	US-11-298-020-7	Sequence 7, Appl
412	102	5.6	273	7	US-11-355-735-15	Sequence 15, Appl	486	94.5	5.2	657	7	US-11-293-697-4607	Sequence 4607, App
413	102	5.6	273	7	US-11-378-707-15	Sequence 15, Appl	487	94.5	5.2	758	7	US-11-191-244-66	Sequence 66, Appl
414	102	5.6	273	7	US-11-346-468-15	Sequence 15, Appl	488	94.5	5.2	2260	7	US-11-375-359-90	Sequence 90, Appl
415	102	5.6	1437	7	US-11-375-359-91	Sequence 91, Appl	489	94.5	5.2	2260	7	US-11-073-360-160	Sequence 160, App
416	101.5	5.6	323	7	US-11-170-797-3	Sequence 3, Appl	490	94.5	5.2	2347	7	US-11-365-989-202	Sequence 202, App
417	101.5	5.6	329	6	US-10-511-937-2520	Sequence 2520, App	491	94.5	5.2	2347	7	US-11-375-359-89	Sequence 89, Appl
418	101.5	5.6	329	7	US-11-326-148-4	Sequence 4, Appl	492	94.5	5.2	2347	7	US-11-073-360-161	Sequence 161, App
419	101.5	5.6	329	7	US-11-364-102-4	Sequence 4, Appl	493	94	5.2	290	7	US-11-355-735-2	Sequence 2, Appl
420	101.5	5.6	466	7	US-11-211-917-70	Sequence 70, Appl	494	94	5.2	290	7	US-11-340-429-4	Sequence 4, Appl
421	101.5	5.6	466	7	US-11-211-917-86	Sequence 86, Appl	495	94	5.2	290	7	US-11-378-707-14	Sequence 14, Appl
422	101.5	5.6	937	7	US-11-365-989-208	Sequence 208, App	496	94	5.2	290	7	US-11-346-468-2	Sequence 2, Appl
423	101	5.6	458	6	US-10-511-937-2504	Sequence 2504, App	497	94	5.2	290	7	US-11-287-573-42	Sequence 42, Appl
424	101	5.6	489	6	US-11-311-754-30	Sequence 30, Appl	498	94	5.2	481	6	US-11-530-035-41	Sequence 41, Appl
425	101	5.6	535	6	US-10-521-319-15	Sequence 15, Appl	499	94	5.2	757	7	US-11-191-244-67	Sequence 67, Appl
426	101	5.6	656	7	US-11-030-653-28	Sequence 38, Appl	500	93.5	5.2	205	7	US-11-346-008-2	Sequence 2, Appl
427	101	5.6	713	7	US-11-030-653-36	Sequence 26, Appl	501	93.5	5.2	205	7	US-11-346-008-5	Sequence 5, Appl
428	100.5	5.6	274	6	US-10-505-928-115	Sequence 115, App	502	93.5	5.2	265	6	US-10-700-439-151	Sequence 151, App
429	100.5	5.6	274	7	US-11-090-997-394	Sequence 394, App	503	93.5	5.2	265	7	US-11-105-233-200	Sequence 200, App
430	100.5	5.6	329	7	US-11-311-754-32	Sequence 32, Appl	504	93.5	5.2	463	7	US-11-375-221-18	Sequence 18, Appl
431	100.5	5.6	449	7	US-11-256-332-158	Sequence 158, App	505	93.5	5.2	465	7	US-11-197-665-12	Sequence 12, Appl
432	100.5	5.6	716	6	US-10-518-039-6	Sequence 6, Appl	506	93	5.1	266	7	US-11-327-917-13	Sequence 13, Appl
433	100.5	5.6	812	6	US-10-518-039-5	Sequence 5, Appl	507	93	5.1	298	6	US-10-669-920-1300	Sequence 1300, App
434	100	5.5	296	7	US-11-311-754-36	Sequence 36, Appl	508	93	5.1	446	7	US-11-197-665-42	Sequence 42, Appl
435	100	5.5	306	7	US-11-311-754-35	Sequence 35, Appl	509	93	5.1	446	7	US-11-197-665-46	Sequence 46, Appl
436	100	5.5	306	7	US-11-313-556-4	Sequence 35, Appl	510	93	5.1	446	7	US-11-197-665-66	Sequence 66, Appl
437	100	5.5	306	7	US-11-359-254-9	GENERAL INFORMA	511	92	5.1	276	7	US-11-359-254-14	Sequence 14, Appl
438	100	5.5	314	7	US-11-170-797-8	Sequence 8, Appl	512	92	5.1	322	7	US-11-311-754-2	Sequence 2, Appl
439	99.5	5.5	260	6	US-10-527-834-2	Sequence 2, Appl	513	92	5.1	322	7	US-11-359-254-7	Sequence 7, Appl
440	99.5	5.5	269	6	US-10-527-100-29	Sequence 29, Appl	514	92	5.1	322	7	US-11-359-254-8	Sequence 8, Appl
441	99.5	5.5	269	7	US-11-090-997-1396	Sequence 1396, App	515	92	5.1	322	7	US-11-359-254-19	Sequence 19, Appl
442	99.5	5.5	733	7	US-11-191-244-70	Sequence 70, Appl	516	92	5.1	328	7	US-11-167-767-29	Sequence 29, Appl
443	99.5	5.5	772	7	US-11-191-244-71	Sequence 71, Appl	517	92	5.1	405	7	US-11-293-697-3958	Sequence 3958, App
444	98.5	5.5	330	7	US-11-170-797-14	Sequence 14, Appl	518	92	5.1	448	7	US-11-317-786B-11	Sequence 11, Appl
445	98.5	5.5	409	6	US-10-505-928-31	Sequence 31, Appl	519	91.5	5.1	457	7	US-11-404-939-579	Sequence 579, App
446	98	5.4	226	7	US-11-183-218-42	Sequence 42, Appl	520	91.5	5.1	461	7	US-11-246-999-44	Sequence 44, Appl
447	98	5.4	771	7	US-11-169-140-13	Sequence 13, Appl	521	91.5	5.1	473	7	US-11-293-697-4278	Sequence 4278, App
448	98	5.4	771	7	US-11-191-244-99	Sequence 99, Appl	522	91.5	5.1	572	7	US-11-269-117-2	Sequence 2, Appl
449	97.5	5.4	269	6	US-10-669-920-753	Sequence 753, App	523	91.5	5.1	4074	6	US-10-501-834-2	Sequence 2, Appl
450	97.5	5.4	315	6	US-10-669-920-755	Sequence 755, App	524	91	5.0	107	7	US-11-370-899-2	Sequence 2, Appl
451	97.5	5.4	316	7	US-11-378-707-4	Sequence 4, Appl	525	91	5.0	107	7	US-11-370-899-2	Sequence 2, Appl
452	97.5	5.4	329	6	US-10-669-920-751	Sequence 751, App	526	91	5.0	107	6	US-10-511-937-2415	Sequence 2415, App
453	97.5	5.4	331	7	US-11-330-768-2	Sequence 2, Appl	527	91	5.0	290	7	US-11-305-843-2	Sequence 2, Appl
454	97.5	5.4	464	7	US-11-211-917-22	Sequence 22, Appl	528	91	5.0	290	7	US-11-305-843-4	Sequence 4, Appl
455	97.5	5.4	557	7	US-11-030-653-12	Sequence 12, Appl	529	91	5.0	480	7	US-11-355-735-5	Sequence 5, Appl
456	97.5	5.4	592	6	US-10-486-020-19	Sequence 19, Appl	530	91	5.0	480	7	US-11-346-468-5	Sequence 5, Appl
457	97.5	5.4	592	7	US-11-030-653-14	Sequence 14, Appl	531	91	5.0	796	7	US-11-361-415-81	Sequence 81, Appl
458	97.5	5.4	316	7	US-11-355-735-13	Sequence 13, Appl	532	90.5	5.0	99	7	US-11-150-871A-189	Sequence 189, App
459	97	5.4	316	7	US-11-378-707-19	Sequence 19, Appl	533	90.5	5.0	282	7	US-11-101-316-60	Sequence 60, Appl
460	97	5.4	316	7	US-11-378-707-19	Sequence 19, Appl	534	90.5	5.0	282	7	US-11-338-537-6	Sequence 6, Appl
461	96.1	5.4	316	7	US-11-346-468-13	Sequence 13, Appl	535	90.5	5.0	282	7	US-11-335-394-6	Sequence 6, Appl
462	96.5	5.3	256	6	US-10-551-504-264	Sequence 264, App	536	90.5	5.0	282	7	US-11-376-697-6	Sequence 6, Appl
463	96.5	5.3	298	6	US-11-043-842-15	Sequence 15, Appl	537	90.5	5.0	306	6	US-10-516-697-6	Sequence 6, Appl
464	96.5	5.3	334	7	US-11-349-852-7	Sequence 7, Appl	538	90.5	5.0	316	7	US-11-154-977-109	Sequence 109, App
465	96.5	5.3	359	7	US-11-349-852-8	Sequence 8, Appl	539	90.5	5.0	343	7	US-11-154-977-99	Sequence 99, Appl
466	96.5	5.3	364	6	US-10-548-681-13	Sequence 13, Appl	540	90.5	5.0	409	7	US-11-222-370-29	Sequence 29, Appl
467	96.5	5.3	518	6	US-10-540-959-1	Sequence 1, Appl	541	90.5	5.0	410	7	US-11-363-149-25	Sequence 25, Appl
468	96.5	5.3	27	7	US-11-134-871-518	Sequence 518, App	542	90.5	5.0	410	7	US-11-363-149-25	Sequence 25, Appl
469	96	5.3	245	7	US-11-340-429-2	Sequence 2, Appl	543	90.5	5.0	446	7	US-11-197-665-89	Sequence 89, Appl
470	96	5.3	347	7	US-11-311-754-4	Sequence 4, Appl	544	90.5	5.0	453	7	US-11-342-353-14	Sequence 14, Appl
471	96	5.3					545	90.5	5.0				

546	90.5	5.0	453	7	US-11-256-332-157	Sequence 157, App	621	86	4.8	450	7	US-11-263-230-222	Sequence 222, App
547	90.5	5.0	461	7	US-11-246-999-119	Sequence 119, App	622	86	4.8	450	7	US-11-375-810-1	Sequence 1, Appli
548	90.5	5.0	500	7	US-11-101-316-84	Sequence 84, Appl	623	86	4.8	460	7	US-11-375-221-14	Sequence 14, Appl
549	90.5	5.0	500	7	US-11-376-673-84	Sequence 84, Appl	624	86	4.8	470	7	US-11-211-917-62	Sequence 62, Appl
550	90.5	5.0	500	7	US-11-073-360-183	Sequence 183, App	625	86	4.8	524	6	US-10-551-504-2	Sequence 2, Appli
551	90.5	5.0	845	6	US-10-669-920-82	Sequence 82, Appl	626	86	4.8	524	6	US-10-551-504-293	Sequence 293, App
552	90.5	5.0	845	6	US-10-669-920-86	Sequence 86, Appl	627	86	4.8	768	6	US-10-449-902-52726	Sequence 52726, A
553	90.5	5.0	1127	6	US-10-547-530-134	Sequence 134, App	628	85.5	4.7	232	7	US-11-373-546-4	Sequence 4, Appli
554	90.5	5.0	1206	6	US-10-547-530-102	Sequence 102, App	629	85.5	4.7	280	7	US-11-288-047-17	Sequence 17, Appli
555	90.5	5.0	1241	6	US-10-547-530-118	Sequence 118, App	630	85.5	4.7	474	6	US-10-560-299-1	Sequence 1, Appli
556	90	5.0	198	7	US-11-090-997-1860	Sequence 1860, Ap	631	85.5	4.7	488	7	US-11-330-403-15240	Sequence 15240, A
558	90	5.0	472	7	US-11-293-697-4295	Sequence 4295, Ap	632	85.5	4.7	764	7	US-11-191-244-65	Sequence 65, Appl
559	90	5.0	606	6	US-10-539-228-816	Sequence 816, App	633	85	4.7	102	6	US-10-538-066-755	Sequence 755, App
560	90	5.0	607	6	US-10-669-920-841	Sequence 841, App	634	85	4.7	214	7	US-11-221-902-11	Sequence 11, Appl
561	90	5.0	607	6	US-10-669-920-843	Sequence 843, App	635	85	4.7	336	6	US-10-516-697-5	Sequence 5, Appli
562	90	5.0	607	6	US-10-669-920-847	Sequence 847, App	636	85	4.7	450	7	US-11-263-230-210	Sequence 210, App
563	90	5.0	2343	6	US-10-540-898-904	Sequence 904, App	637	85	4.7	450	7	US-11-263-230-218	Sequence 218, App
564	89.5	5.0	254	7	US-11-305-843-6	Sequence 6, Appli	638	85	4.7	450	7	US-11-263-230-220	Sequence 220, App
565	89.5	5.0	254	7	US-11-305-843-10	Sequence 10, Appl	639	85	4.7	450	7	US-11-263-230-230	Sequence 230, App
566	89.5	5.0	342	7	US-11-293-697-3183	Sequence 3183, Ap	640	85	4.7	450	7	US-11-263-230-240	Sequence 240, App
567	89.5	5.0	446	7	US-11-197-665-62	Sequence 62, Appl	641	85	4.7	450	7	US-11-263-230-250	Sequence 250, App
568	89	4.9	277	7	US-11-177-495-3	Sequence 3, Appli	642	85	4.7	450	7	US-11-337-300-472	Sequence 472, App
569	89	4.9	769	7	US-11-191-244-69	Sequence 69, Appl	643	85	4.7	469	7	US-11-295-006-15	Sequence 15, Appl
570	88.5	4.9	304	6	US-10-669-920-546	Sequence 546, App	644	85	4.7	788	7	US-11-211-917-78	Sequence 78, Appl
571	88.5	4.9	309	7	US-11-311-754-33	Sequence 33, Appl	645	85	4.7	1060	6	US-11-188-417A-30	Sequence 30, Appl
572	88.5	4.9	309	7	US-11-170-797-10	Sequence 10, Appl	646	85	4.7	251	7	US-10-505-928-729	Sequence 729, App
573	88.5	4.9	319	7	US-11-246-999-37	Sequence 37, Appl	647	84.5	4.7	328	6	US-11-337-300-222	Sequence 222, App
574	88.5	4.9	329	7	US-11-414-707-6	Sequence 6, Appli	648	84.5	4.7	328	6	US-10-505-928-597	Sequence 597, App
575	88.5	4.9	332	7	US-11-288-047-26	Sequence 26, Appl	649	84.5	4.7	385	6	US-10-953-349-3765	Sequence 3765, Ap
576	88.5	4.9	446	7	US-11-197-665-54	Sequence 54, Appl	650	84.5	4.7	385	6	US-11-056-355B-35194	Sequence 35194, A
577	88.5	4.9	449	7	US-11-256-332-154	Sequence 154, App	651	84.5	4.7	385	7	US-11-056-355B-101617	Sequence 101617, A
578	88.5	4.9	449	7	US-11-256-332-155	Sequence 155, App	652	84.5	4.7	385	7	US-11-056-355B-112856	Sequence 112856, A
579	88.5	4.9	451	6	US-10-822-231-1	Sequence 1, Appli	653	84.5	4.7	392	7	US-11-056-355B-101616	Sequence 101616, A
580	88.5	4.9	461	7	US-11-375-221-66	Sequence 66, Appl	654	84.5	4.7	392	7	US-11-056-355B-112855	Sequence 112855, A
582	88.5	4.9	466	7	US-11-101-316-104	Sequence 104, App	655	84.5	4.7	414	7	US-11-056-355B-71293	Sequence 71293, A
583	88.5	4.9	466	7	US-11-376-673-104	Sequence 104, App	656	84.5	4.7	449	7	US-11-256-332-169	Sequence 169, App
584	88.5	4.9	556	7	US-11-441-780-4	Sequence 4, Appli	657	84.5	4.7	449	7	US-11-256-332-170	Sequence 170, App
585	88	4.9	279	7	US-11-287-573-44	Sequence 44, Appl	658	84.5	4.7	465	7	US-11-211-917-38	Sequence 38, Appl
586	88	4.9	290	7	US-11-340-429-11	Sequence 11, Appl	659	84.5	4.7	491	7	US-11-293-697-4290	Sequence 4290, Ap
587	88	4.9	442	7	US-11-090-997-296	Sequence 296, App	660	84.5	4.7	527	7	US-11-056-355B-71291	Sequence 71291, A
588	88	4.9	447	7	US-11-361-528-1	Sequence 1, Appli	661	84.5	4.7	596	7	US-11-056-355B-71290	Sequence 71290, A
589	88	4.9	448	7	US-11-317-786B-7	Sequence 7, Appli	662	84.5	4.7	727	7	US-11-251-308-228	Sequence 228, App
590	88	4.9	450	7	US-11-197-665-34	Sequence 34, Appl	663	84	4.7	68	7	US-11-175-714-61	Sequence 61, Appl
591	88	4.9	450	7	US-11-197-665-38	Sequence 38, Appl	664	84	4.7	102	7	US-11-150-871A-196	Sequence 196, App
592	87.5	4.8	289	7	US-11-154-977-103	Sequence 103, App	665	84	4.7	237	7	US-11-305-843-8	Sequence 8, Appli
593	87.5	4.8	408	6	US-10-449-902-42795	Sequence 42795, A	666	84	4.7	251	6	US-10-537-143-2	Sequence 2, Appli
594	87.5	4.8	446	7	US-11-197-665-58	Sequence 58, Appl	667	84	4.7	260	6	US-10-991-309B-160	Sequence 160, App
595	87.5	4.8	532	6	US-10-953-349-23102	Sequence 23102, A	668	84	4.7	267	7	US-11-447-460-19	Sequence 19, Appl
596	87.5	4.8	534	6	US-10-953-349-23101	Sequence 23101, A	669	84	4.7	313	7	US-11-447-460-16	Sequence 16, Appl
597	87.5	4.8	537	6	US-10-953-349-23100	Sequence 23100, A	670	84	4.7	450	7	US-11-263-230-214	Sequence 214, App
598	87	4.8	357	7	US-11-056-355B-12438	Sequence 12438, A	671	84	4.7	450	7	US-11-263-230-216	Sequence 216, App
599	87	4.8	392	7	US-11-056-355B-12437	Sequence 12437, A	672	84	4.7	454	7	US-11-256-332-160	Sequence 160, App
600	87	4.8	401	7	US-11-056-355B-12436	Sequence 12436, A	673	84	4.7	464	7	US-11-375-221-22	Sequence 22, Appl
601	87	4.8	518	7	US-11-056-355B-47684	Sequence 47684, A	674	84	4.7	473	7	US-11-293-697-4284	Sequence 4284, Ap
602	87	4.8	547	7	US-11-056-355B-47683	Sequence 47683, A	675	84	4.7	524	6	US-10-551-504-254	Sequence 254, App
603	87	4.8	566	7	US-11-056-355B-47682	Sequence 47682, A	676	84	4.7	612	6	US-10-537-143-4	Sequence 4, Appli
604	87	4.8	1018	7	US-11-090-997-1478	Sequence 1478, Ap	677	84	4.7	1159	6	US-10-547-530-132	Sequence 132, App
605	86.5	4.8	304	7	US-11-294-448-2	Sequence 2, Appli	678	84	4.7	1238	6	US-10-547-530-100	Sequence 100, App
606	86.5	4.8	319	6	US-10-669-920-551	Sequence 551, App	679	84	4.7	1273	6	US-10-547-530-116	Sequence 116, App
607	86.5	4.8	325	6	US-10-669-920-549	Sequence 549, App	680	83.5	4.6	255	6	US-10-548-727-8	Sequence 8, Appli
608	86.5	4.8	799	7	US-11-361-415-82	Sequence 82, Appl	681	83.5	4.6	299	7	US-11-265-762-144	Sequence 144, App
609	86.5	4.8	2804	7	US-11-330-403-12380	Sequence 12380, A	682	83.5	4.6	328	7	US-11-441-780-2	Sequence 2, Appli
610	86	4.8	217	6	US-10-953-349-34469	Sequence 34469, A	683	83.5	4.6	367	7	US-11-330-403-7428	Sequence 7428, Ap
611	86	4.8	217	6	US-11-056-355B-7902	Sequence 7902, Ap	684	83.5	4.6	461	7	US-11-375-221-34	Sequence 34, Appl
612	86	4.8	234	6	US-11-375-221-12	Sequence 12, Appli	685	83.5	4.6	513	7	US-11-056-355B-70628	Sequence 70628, A
613	86	4.8	236	6	US-10-529-072-2	Sequence 2, Appli	686	83.5	4.6	541	7	US-11-330-403-13809	Sequence 13809, A
614	86	4.8	254	6	US-10-553-105-28	Sequence 28, Appl	687	83.5	4.6	549	7	US-11-056-355B-72608	Sequence 72608, A
615	86	4.8	264	6	US-10-541-708-32	Sequence 32, Appl	688	83.5	4.6	631	7	US-11-056-355B-72607	Sequence 72607, A
616	86	4.8	308	6	US-10-953-349-34468	Sequence 34468, A	689	83.5	4.6	632	7	US-11-174-307B-140	Sequence 140, App
617	86	4.8	308	6	US-11-056-355B-7901	Sequence 7901, Ap	690	83.5	4.6	632	7	US-11-056-355B-72606	Sequence 72606, A
618	86	4.8	329	6	US-10-669-920-748	Sequence 748, App	691	83.5	4.6	4834	6	US-10-505-928-827	Sequence 827, App
619	86	4.8	329	7	US-11-369-229-2	Sequence 2, Appli	692	83	4.6	107	7	US-11-370-899-4	Sequence 4, Appli
620	86	4.8	450	7	US-11-263-230-208	Sequence 208, App	693	83	4.6	107	7	US-11-370-898-4	Sequence 4, Appli

694	83	4.6	225	6	US-10-471-571A-488	Sequence 488, App	768	81	4.5	262	6	US-10-541-708-34	Sequence 34, Appl
695	83	4.6	270	7	US-11-317-435-2	Sequence 2, Appli	769	81	4.5	285	7	US-11-073-360-128	Sequence 128, App
696	83	4.6	292	7	US-11-447-460-18	Sequence 18, Appl	770	81	4.5	335	7	US-11-167-767-25	Sequence 25, Appl
698	83	4.6	381	7	US-11-056-355B-17524	Sequence 17524, A	771	81	4.5	376	6	US-10-538-231-7	Sequence 7, Appli
699	83	4.6	448	7	US-11-317-786B-9	Sequence 9, Appli	772	81	4.5	401	7	US-11-330-403-11685	Sequence 11685, A
700	83	4.6	450	7	US-11-263-230-224	Sequence 224, App	773	81	4.5	446	7	US-11-056-355B-48124	Sequence 48124, A
701	83	4.6	450	7	US-11-263-230-226	Sequence 226, App	774	81	4.5	462	7	US-11-375-221-50	Sequence 50, Appl
702	83	4.6	450	7	US-11-263-230-228	Sequence 228, App	775	81	4.5	464	7	US-11-056-355B-48123	Sequence 48123, A
703	83	4.6	450	7	US-11-263-230-232	Sequence 232, App	776	81	4.5	575	7	US-11-056-355B-48122	Sequence 48122, A
704	83	4.6	450	7	US-11-263-230-234	Sequence 234, App	777	81	4.5	1344	6	US-10-805-394-6888	Sequence 6888, Ap
705	83	4.6	450	7	US-11-263-230-236	Sequence 236, App	778	80.5	4.5	57	7	US-11-175-714-63	Sequence 63, Appl
706	83	4.6	450	7	US-11-263-230-238	Sequence 238, App	779	80.5	4.5	223	6	US-10-525-365-15	Sequence 15, Appl
707	83	4.6	450	7	US-11-263-230-242	Sequence 242, App	780	80.5	4.5	239	7	US-11-211-917-80	Sequence 80, Appl
708	83	4.6	450	7	US-11-263-230-244	Sequence 244, App	781	80.5	4.5	286	7	US-11-154-103-8	Sequence 8, Appli
709	83	4.6	450	7	US-11-263-230-246	Sequence 246, App	782	80.5	4.5	531	7	US-11-418-058-10	Sequence 10, Appl
710	83	4.6	450	7	US-11-263-230-248	Sequence 248, App	783	80.5	4.5	535	7	US-11-293-697-4247	Sequence 4247, Ap
711	83	4.6	450	7	US-11-263-230-252	Sequence 252, App	784	80	4.4	245	7	US-11-337-300-53	Sequence 53, Appl
712	83	4.6	450	7	US-11-263-230-254	Sequence 254, App	785	80	4.4	249	7	US-11-337-300-90	Sequence 90, Appl
713	83	4.6	450	7	US-11-263-230-256	Sequence 256, App	786	80	4.4	283	6	US-10-504-973-13	Sequence 13, Appl
714	83	4.6	450	7	US-11-263-230-303	Sequence 303, App	787	80	4.4	329	7	US-11-288-047-7	Sequence 7, Appli
715	83	4.6	450	7	US-11-263-230-309	Sequence 309, App	788	80	4.4	342	6	US-10-449-902-28675	Sequence 28675, A
716	83	4.6	450	7	US-11-263-230-316	Sequence 316, App	789	80	4.4	342	6	US-10-449-902-30350	Sequence 30350, A
717	83	4.6	450	7	US-11-263-230-322	Sequence 322, App	790	80	4.4	342	6	US-10-449-902-32589	Sequence 32589, A
718	83	4.6	450	7	US-11-263-230-327	Sequence 327, App	791	80	4.4	342	6	US-10-449-902-52982	Sequence 52982, A
719	83	4.6	450	7	US-11-375-810-11	Sequence 11, Appl	792	80	4.4	460	7	US-11-375-221-26	Sequence 26, Appl
720	83	4.6	473	7	US-11-290-687-29	Sequence 29, Appl	793	80	4.4	460	7	US-11-375-221-74	Sequence 74, Appl
721	83	4.6	480	7	US-11-056-355B-17523	Sequence 17523, A	794	80	4.4	469	7	US-11-211-917-54	Sequence 54, Appl
722	83	4.6	524	6	US-10-551-504-260	Sequence 260, App	795	80	4.4	504	6	US-10-504-973-5	Sequence 5, Appli
723	83	4.6	631	6	US-10-374-780A-513	Sequence 513, App	796	80	4.4	524	6	US-10-551-504-287	Sequence 287, App
724	83	4.6	650	6	US-10-374-780A-514	Sequence 514, App	797	80	4.4	554	7	US-11-050-113-19	Sequence 19, Appl
725	83	4.6	674	6	US-10-449-902-43418	Sequence 43418, A	798	80	4.4	572	7	US-11-056-355B-90991	Sequence 90991, A
726	83	4.6	1321	7	US-11-300-928-49	Sequence 49, Appl	799	80	4.4	572	7	US-11-056-355B-94747	Sequence 94747, A
727	83	4.6	2972	7	US-11-330-403-15100	Sequence 15100, A	800	80	4.4	671	6	US-10-449-902-35887	Sequence 35887, A
728	83	4.6	4590	6	US-10-505-928-569	Sequence 569, App	801	80	4.4	891	6	US-10-449-902-54504	Sequence 54504, A
729	82.5	4.6	213	6	US-10-953-349-34470	Sequence 34470, A	802	80	4.4	1629	6	US-10-471-571A-3542	Sequence 3542, Ap
730	82.5	4.6	213	7	US-11-056-355B-7903	Sequence 7903, Ap	803	79.5	4.4	126	7	US-11-154-977-5	Sequence 5, Appli
731	82.5	4.6	273	6	US-10-471-571A-2862	Sequence 2862, Ap	804	79.5	4.4	167	7	US-11-056-355B-30197	Sequence 30197, A
732	82.5	4.6	286	6	US-10-991-309B-162	Sequence 162, App	805	79.5	4.4	167	7	US-11-056-355B-33787	Sequence 33787, A
733	82.5	4.6	314	6	US-10-449-902-45045	Sequence 45045, A	806	79.5	4.4	213	7	US-11-301-373-51	Sequence 51, Appl
734	82.5	4.6	303	6	US-10-981-300-16	Sequence 16, Appl	807	79.5	4.4	223	6	US-10-525-365-17	Sequence 17, Appl
735	82.5	4.6	454	7	US-11-290-687-32	Sequence 32, Appl	808	79.5	4.4	247	6	US-10-541-708-45	Sequence 45, Appl
736	82.5	4.6	470	7	US-11-233-697-4684	Sequence 4684, Ap	809	79.5	4.4	416	6	US-10-449-902-33321	Sequence 33321, A
737	82.5	4.6	500	7	US-11-233-697-4684	Sequence 4684, Ap	811	79.5	4.4	428	6	US-10-449-902-42681	Sequence 42681, A
738	82.5	4.6	556	6	US-10-449-902-35255	Sequence 35255, A	812	79.5	4.4	434	6	US-10-538-231-5	Sequence 5, Appli
739	82.5	4.6	1263	6	US-10-471-571A-5118	Sequence 5118, Ap	813	79.5	4.4	445	7	US-11-021-819A-16	Sequence 16, Appl
740	82.5	4.6	4059	6	US-11-501-834-6	Sequence 6, Appli	815	79.5	4.4	463	7	US-11-101-316-86	Sequence 86, Appl
741	82	4.5	99	7	US-11-150-871A-176	Sequence 176, App	816	79.5	4.4	463	7	US-11-376-673-86	Sequence 86, Appl
742	82	4.5	144	7	US-11-154-977-77	Sequence 77, Appl	817	79.5	4.4	464	7	US-11-021-819A-62	Sequence 62, Appl
743	82	4.5	171	7	US-11-154-977-67	Sequence 67, Appl	818	79.5	4.4	613	7	US-11-434-137-204	Sequence 204, App
744	82	4.5	250	6	US-10-521-109-6	Sequence 67, Appl	819	79.5	4.4	613	7	US-11-434-184-204	Sequence 204, App
745	82	4.5	283	7	US-11-293-697-4639	Sequence 4639, Ap	820	79.5	4.4	613	7	US-11-434-199-204	Sequence 204, App
746	82	4.5	288	6	US-10-511-937-2409	Sequence 2409, Ap	821	79.5	4.4	613	7	US-11-434-203-204	Sequence 204, App
747	82	4.5	288	7	US-11-311-754-34	Sequence 34, Appl	822	79.5	4.4	688	6	US-10-514-738-33	Sequence 33, Appl
748	82	4.5	288	7	US-11-313-556-2	GENERAL INFORMA	823	79.5	4.4	766	6	US-10-514-738-2	Sequence 2, Appli
749	82	4.5	288	7	US-11-326-148-2	Sequence 2, Appli	824	79.5	4.4	766	6	US-10-514-738-4	Sequence 4, Appli
750	82	4.5	288	7	US-11-170-797-1	Sequence 1, Appli	825	79.5	4.4	766	6	US-10-514-738-35	Sequence 35, Appl
751	82	4.5	288	7	US-11-364-102-2	Sequence 2, Appli	826	79.5	4.4	1161	7	US-11-192-046-121	Sequence 121, App
752	82	4.5	442	7	US-11-197-712-286	Sequence 286, App	827	79	4.4	107	7	US-11-221-902-23	Sequence 23, Appl
753	82	4.5	450	7	US-11-263-230-212	Sequence 212, App	828	79	4.4	348	7	US-11-330-403-3634	Sequence 3634, Ap
754	82	4.5	461	7	US-11-167-767-44	Sequence 44, Appl	829	79	4.4	443	7	US-11-056-355B-81684	Sequence 81684, A
755	82	4.5	468	7	US-11-197-712-283	Sequence 283, App	830	79	4.4	450	7	US-11-303-478-54	Sequence 54, Appl
756	82	4.5	660	6	US-10-449-902-42505	Sequence 42505, A	831	79	4.4	452	7	US-11-256-332-168	Sequence 168, App
757	81.5	4.5	128	7	US-11-224-664-34	Sequence 34, Appl	832	79	4.4	461	7	US-11-375-221-2	Sequence 2, Appli
758	81.5	4.5	288	7	US-11-154-103-3	Sequence 3, Appli	833	79	4.4	464	6	US-10-669-920-1407	Sequence 1407, Ap
759	81.5	4.5	291	7	US-11-154-977-27	Sequence 27, Appl	834	79	4.4	468	7	US-11-232-150-2	Sequence 2, Appli
760	81.5	4.5	453	7	US-11-154-977-32	Sequence 32, App	835	79	4.4	745	7	US-11-293-697-3826	Sequence 3826, Ap
761	81.5	4.5	623	6	US-10-449-902-56221	Sequence 56221, A	836	79	4.4	767	7	US-11-090-997-636	Sequence 636, App
762	81.5	4.5	2152	6	US-10-544-944-1	Sequence 1, Appli	837	79	4.4	778	7	US-11-090-997-634	Sequence 634, App
763	81	4.5	140	7	US-11-154-977-141	Sequence 141, App	838	79	4.4	1318	6	US-10-449-902-52857	Sequence 52857, A
764	81	4.5	167	7	US-11-154-977-131	Sequence 131, App	839	78.5	4.3	140	6	US-11-154-977-123	Sequence 123, App
765	81	4.5	234	6	US-10-541-708-33	Sequence 33, Appl	840	78.5	4.3	204	6	US-10-805-394-4542	Sequence 4542, Ap
766	81	4.5	249	6	US-10-553-105-36	Sequence 36, Appl	841	78.5	4.3	213	6	US-10-822-231-3	Sequence 3, Appli
767	81	4.5	252	7	US-11-073-360-127	Sequence 127, App	842	78.5	4.3	213	7	US-11-174-287-6	Sequence 6, Appli

843	78.5	4.3	213	7	US-11-256-060-16	Sequence 16, Appl	916	77	4.3	484	7	US-11-056-355B-104780	Sequence 104780,
844	78.5	4.3	212	7	US-11-274-452-1	Sequence 1, Appl	917	77	4.3	484	7	US-11-056-355B-116019	Sequence 116019,
845	78.5	4.3	232	6	US-10-560-299-6	Sequence 6, Appl	918	77	4.3	499	7	US-11-342-171-8	Sequence 8, Appl
846	78.5	4.3	238	6	US-10-526-741-20	Sequence 20, Appl	919	77	4.3	499	7	US-11-342-171-8	Sequence 69, Appl
847	78.5	4.3	238	7	US-11-414-676-20	Sequence 20, Appl	920	77	4.3	562	7	US-11-056-355B-78403	Sequence 78403, A
848	78.5	4.3	239	7	US-11-211-917-16	Sequence 16, Appl	921	77	4.3	584	6	US-10-471-571A-1336	Sequence 1336, Ap
849	78.5	4.3	239	7	US-11-211-917-56	Sequence 56, Appl	922	77	4.3	591	7	US-11-056-355B-78402	Sequence 78402, A
850	78.5	4.3	243	7	US-11-075-891-4	Sequence 4, Appl	923	77	4.3	610	7	US-11-056-355B-78401	Sequence 78401, A
851	78.5	4.3	295	7	US-11-274-452-7	Sequence 7, Appl	924	77	4.3	671	6	US-10-449-902-53976	Sequence 53976, A
852	78.5	4.3	316	7	US-11-154-977-91	Sequence 91, Appl	925	76.5	4.2	110	7	US-11-328-483-67	Sequence 67, Appl
853	78.5	4.3	437	7	US-11-163-586-71	Sequence 71, Appl	926	76.5	4.2	115	7	US-11-094-132-77	Sequence 77, Appl
854	78.5	4.3	445	7	US-11-317-786B-32	Sequence 32, Appl	927	76.5	4.2	129	6	US-10-513-148A-4	Sequence 4, Appl
855	78.5	4.3	453	7	US-11-256-332-152	Sequence 152, App	928	76.5	4.2	208	7	US-11-330-403-14192	Sequence 14192, A
856	78.5	4.3	453	7	US-11-256-332-153	Sequence 153, App	929	76.5	4.2	234	7	US-11-232-150-4	Sequence 4, Appl
857	78.5	4.3	453	7	US-11-256-332-173	Sequence 173, App	930	76.5	4.2	235	7	US-11-290-687-26	Sequence 26, Appl
858	78.5	4.3	453	7	US-11-256-332-174	Sequence 174, App	931	76.5	4.2	239	7	US-11-412-325-8	Sequence 8, Appl
859	78.5	4.3	461	7	US-11-375-221-70	Sequence 70, Appl	932	76.5	4.2	258	6	US-10-541-708-21	Sequence 21, Appl
860	78.5	4.3	470	7	US-11-290-687-30	Sequence 30, Appl	933	76.5	4.2	358	6	US-10-471-571A-5542	Sequence 5542, Ap
861	78.5	4.3	502	7	US-11-290-687-33	Sequence 33, Appl	934	76.5	4.2	652	7	US-11-330-403-12464	Sequence 12464, A
862	78.5	4.3	613	7	US-11-293-697-4245	Sequence 4245, Ap	935	76.5	4.2	788	6	US-10-449-902-41268	Sequence 41268, A
863	78.5	4.3	613	7	US-11-434-137-206	Sequence 206, App	936	76.5	4.2	857	6	US-10-669-920-75	Sequence 75, Appl
864	78.5	4.3	613	7	US-11-434-184-206	Sequence 206, App	937	76.5	4.2	857	6	US-10-669-920-77	Sequence 77, Appl
865	78.5	4.3	613	7	US-11-434-199-206	Sequence 206, App	938	76.5	4.2	857	6	US-10-669-920-79	Sequence 79, Appl
866	78.5	4.3	613	7	US-11-434-203-206	Sequence 206, App	939	76.5	4.2	874	7	US-11-056-355B-78161	Sequence 78161, A
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868	78	4.3	118	7	US-11-293-697-4517	Sequence 4517, Ap	941	76.5	4.2	1124	7	US-11-365-989-190	Sequence 190, App
869	78	4.3	214	7	US-11-221-902-5	Sequence 5, Appl	942	76.5	4.2	1686	7	US-11-233-174-8	Sequence 8, Appl
870	78	4.3	214	7	US-11-221-902-7	Sequence 7, Appl	943	76	4.2	66	7	US-11-175-714-64	Sequence 64, Appl
871	78	4.3	214	7	US-11-221-902-9	Sequence 9, Appl	944	76	4.2	117	7	US-11-413-563-32	Sequence 32, Appl
872	78	4.3	235	7	US-11-288-047-12	Sequence 12, Appl	945	76	4.2	206	6	US-10-530-035-37	Sequence 37, Appl
873	78	4.3	245	7	US-11-337-300-59	Sequence 59, Appl	946	76	4.2	238	6	US-11-298-020-10	Sequence 10, Appl
874	78	4.3	248	6	US-10-553-105-32	Sequence 32, Appl	947	76	4.2	239	6	US-10-669-920-260	Sequence 260, App
875	78	4.3	277	6	US-10-449-902-47381	Sequence 47381, A	948	76	4.2	245	7	US-11-337-300-63	Sequence 63, Appl
876	78	4.3	291	7	US-11-154-103-10	Sequence 10, Appl	949	76	4.2	249	7	US-11-167-773-53	Sequence 53, Appl
877	78	4.3	296	7	US-11-169-140-12	Sequence 12, Appl	950	76	4.2	249	7	US-11-167-773-72	Sequence 72, Appl
878	78	4.3	301	7	US-11-317-571-74	Sequence 74, Appl	951	76	4.2	249	7	US-11-321-894-8	Sequence 8, Appl
879	78	4.3	304	7	US-11-288-047-2	Sequence 2, Appl	952	76	4.2	290	7	US-11-154-103-4	Sequence 4, Appl
880	78	4.3	365	6	US-10-511-937-2330	Sequence 2330, Ap	953	76	4.2	296	7	US-11-265-762-152	Sequence 152, App
881	78	4.3	365	7	US-11-090-997-2008	Sequence 2008, Ap	954	76	4.2	310	6	US-10-471-571A-2282	Sequence 2282, Ap
882	78	4.3	450	7	US-11-303-478-52	Sequence 52, Appl	955	76	4.2	326	6	US-10-449-902-33835	Sequence 33835, A
883	78	4.3	636	6	US-10-449-902-44935	Sequence 44935, A	956	76	4.2	358	6	US-10-464-795-15	Sequence 15, Appl
884	78	4.3	730	6	US-10-449-902-51873	Sequence 51873, A	957	76	4.2	450	7	US-11-221-902-2	Sequence 2, Appl
885	78	4.3	859	7	US-11-429-276-432	Sequence 432, App	958	76	4.2	451	7	US-11-256-332-164	Sequence 164, App
886	78	4.3	1016	7	US-11-450-517-95	Sequence 95, Appl	959	76	4.2	462	7	US-11-375-221-46	Sequence 46, Appl
887	78	4.3	1138	7	US-11-365-989-188	Sequence 188, App	960	76	4.2	462	7	US-11-375-221-86	Sequence 86, Appl
888	78	4.3	249	6	US-10-991-309B-176	Sequence 176, App	961	76	4.2	497	7	US-11-056-355B-52675	Sequence 52675, A
889	77.5	4.3	325	7	US-11-429-276-648	Sequence 648, App	962	76	4.2	506	7	US-11-258-363-2	Sequence 2, Appl
890	77.5	4.3	325	7	US-11-090-997-1402	Sequence 1402, Ap	963	76	4.2	544	7	US-11-257-581-2	Sequence 2, Appl
891	77.5	4.3	331	6	US-10-449-902-23310	Sequence 23310, A	964	76	4.2	544	7	US-11-257-579-2	Sequence 2, Appl
892	77.5	4.3	336	7	US-11-369-229-4	Sequence 29310, A	965	76	4.2	560	6	US-10-449-902-55344	Sequence 55344, A
893	77.5	4.3	428	7	US-11-056-355B-83409	Sequence 83409, A	966	76	4.2	570	7	US-11-056-355B-52674	Sequence 52674, A
894	77.5	4.3	463	7	US-11-375-221-6	Sequence 6, Appl	967	76	4.2	600	7	US-11-056-355B-52673	Sequence 52673, A
895	77.5	4.3	470	6	US-10-539-228-834	Sequence 834, App	968	76	4.2	716	7	US-11-293-697-3834	Sequence 3834, Ap
896	77.5	4.3	470	7	US-11-293-697-4292	Sequence 4292, Ap	969	76	4.2	837	7	US-11-056-355B-108275	Sequence 108275,
897	77.5	4.3	470	7	US-11-293-697-4292	Sequence 3971, Ap	970	76	4.2	837	7	US-11-056-355B-119514	Sequence 119514,
898	77.5	4.3	609	7	US-11-293-697-3371	Sequence 907, App	971	76	4.2	1234	6	US-10-953-349-3997	Sequence 3997, Ap
899	77.5	4.3	128	7	US-10-540-898-907	Sequence 907, App	972	76	4.2	1234	6	US-11-056-355B-36918	Sequence 36918, A
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901	77	4.3	248	6	US-10-953-349-3412	Sequence 3412, Ap	974	76	4.2	1234	7	US-11-056-355B-116722	Sequence 116722,
902	77	4.3	320	7	US-11-056-355B-77955	Sequence 77955, A	975	76	4.2	1237	6	US-10-953-349-3996	Sequence 3996, Ap
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904	77	4.3	320	7	US-11-056-355B-116020	Sequence 116020,	977	76	4.2	1237	7	US-11-056-355B-105482	Sequence 105482,
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907	77	4.3	417	6	US-10-953-349-3412	Sequence 3412, Ap	980	76	4.2	1337	7	US-11-056-355B-36916	Sequence 36916, A
908	77	4.3	423	6	US-10-953-349-3411	Sequence 3411, Ap	981	76	4.2	1337	7	US-11-056-355B-105481	Sequence 105481,
909	77	4.3	467	7	US-11-293-697-4293	Sequence 4293, Ap	982	76	4.2	1337	7	US-11-056-355B-116720	Sequence 116720,
910	77	4.3	467	7	US-11-293-697-4293	Sequence 70629, A	983	76	4.2	1386	6	US-10-449-902-48092	Sequence 48092, A
911	77	4.3	467	7	US-11-056-355B-70629	Sequence 70629, A	984	76	4.2	1386	6	US-10-449-902-48092	Sequence 48092, A
912	77	4.3	469	7	US-11-293-697-4287	Sequence 4287, Ap	985	75.5	4.2	141	7	US-10-513-148A-16	Sequence 16, Appl
913	77	4.3	474	7	US-11-293-697-4282	Sequence 4282, Ap	986	75.5	4.2	141	7	US-11-324-769-16	Sequence 16, Appl
914	77	4.3	474	7	US-11-293-697-4282	Sequence 4282, Ap	987	75.5	4.2	144	7	US-11-154-977-59	Sequence 59, Appl
915	77	4.3	484	7	US-11-056-355B-77954	Sequence 77954, A	988	75.5	4.2	236	7	US-11-293-697-4281	Sequence 4281, Ap

989	75.5	4.2	239	7	US-11-211-917-8	Sequence 8, Appli	1062	74.5	4.1	434	7	US-11-434-184-952	Sequence 952, App
990	75.5	4.2	239	7	US-11-211-917-64	Sequence 64, Appli	1063	74.5	4.1	434	7	US-11-434-199-952	Sequence 952, App
991	75.5	4.2	244	7	US-11-402-010-77	Sequence 77, Appli	1064	74.5	4.1	434	7	US-11-434-203-952	Sequence 952, App
992	75.5	4.2	248	7	US-11-056-355B-70713	Sequence 70713, A	1065	74.5	4.1	446	6	US-10-953-349-5903	Sequence 5903, App
993	75.5	4.2	249	6	US-10-553-105-30	Sequence 30, Appli	1066	74.5	4.1	453	7	US-11-256-332-167	Sequence 167, App
994	75.5	4.2	271	6	US-10-449-902-33243	Sequence 33243, A	1067	74.5	4.1	470	6	US-10-526-741-16	Sequence 16, Appli
995	75.5	4.2	279	6	US-10-968-757-2	Sequence 2, Appli	1068	74.5	4.1	470	7	US-11-290-687-31	Sequence 31, Appli
996	75.5	4.2	305	7	US-11-330-403-3932	Sequence 3932, Ap	1069	74.5	4.1	470	7	US-11-414-676-16	Sequence 16, Appli
997	75.5	4.2	341	7	US-11-330-403-3197	Sequence 3197, Ap	1070	74.5	4.1	496	7	US-11-293-697-4058	Sequence 4058, Ap
998	75.5	4.2	359	6	US-10-449-902-48132	Sequence 48132, A	1071	74.5	4.1	541	6	US-10-807-997-4	Sequence 4, Appli
999	75.5	4.2	433	7	US-11-293-697-3439	Sequence 3439, Ap	1072	74.5	4.1	541	7	US-11-256-499A-4	Sequence 4, Appli
1000	75.5	4.2	447	7	US-11-221-902-6	Sequence 4, Appli	1073	74.5	4.1	590	6	US-11-350-375A-4	Sequence 4, Appli
1001	75.5	4.2	447	7	US-11-221-902-4	Sequence 6, Appli	1074	74.5	4.1	590	6	US-10-953-349-5902	Sequence 5902, Ap
1002	75.5	4.2	447	7	US-11-303-478-53	Sequence 53, Appli	1075	74.5	4.1	644	6	US-10-953-349-5901	Sequence 5901, Ap
1003	75.5	4.2	448	7	US-11-183-218-56	Sequence 56, Appli	1076	74.5	4.1	749	6	US-10-449-902-4186	Sequence 4186, A
1004	75.5	4.2	456	7	US-11-330-403-17952	Sequence 17952, A	1077	74.5	4.1	898	7	US-11-370-424-5	Sequence 5, Appli
1005	75.5	4.2	471	7	US-11-211-917-6	Sequence 6, Appli	1078	74.5	4.1	2835	6	US-10-509-024-2	Sequence 2, Appli
1006	75.5	4.2	495	7	US-11-293-697-4277	Sequence 6, Appli	1079	74	4.1	240	7	US-11-375-221-24	Sequence 24, Appli
1007	75.5	4.2	516	7	US-11-293-697-4452	Sequence 4452, Ap	1080	74	4.1	243	7	US-11-337-300-47	Sequence 47, Appli
1008	75.5	4.2	567	7	US-11-303-478-55	Sequence 55, Appli	1081	74	4.1	247	7	US-11-337-300-96	Sequence 96, Appli
1009	75.5	4.2	685	7	US-11-188-417A-44	Sequence 44, Appli	1082	74	4.1	304	7	US-11-388-304-12	Sequence 12, Appli
1010	75.5	4.2	746	6	US-10-553-928-295	Sequence 295, App	1083	74	4.1	361	6	US-10-449-902-54139	Sequence 54139, A
1011	75.5	4.2	765	7	US-11-165-586-36	Sequence 36, Appli	1084	74	4.1	442	7	US-11-090-997-1248	Sequence 1248, A
1012	75.5	4.2	1165	7	US-11-377-486-56	Sequence 56, Appli	1085	74	4.1	445	6	US-10-449-902-42824	Sequence 42824, A
1013	75	4.2	87	7	US-11-370-899-17	Sequence 17, Appli	1086	74	4.1	447	7	US-11-256-332-162	Sequence 162, App
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1015	75	4.2	106	7	US-11-256-060-1	Sequence 1, Appli	1088	74	4.1	484	7	US-11-434-184-2938	Sequence 2938, Ap
1016	75	4.2	128	7	US-11-290-687-8	Sequence 8, Appli	1089	74	4.1	484	7	US-11-434-199-2938	Sequence 2938, Ap
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1018	75	4.2	220	7	US-11-118-112A-118	Sequence 118, App	1091	74	4.1	514	6	US-10-471-571A-4680	Sequence 4680, Ap
1019	75	4.2	234	6	US-10-560-299-2	Sequence 2, Appli	1092	74	4.1	514	6	US-10-539-228-831	Sequence 831, App
1020	75	4.2	237	7	US-11-106-762-8	Sequence 8, Appli	1093	74	4.1	577	6	US-10-449-902-44429	Sequence 44429, A
1021	75	4.2	242	6	US-10-541-708-11	Sequence 11, Appli	1094	74	4.1	577	6	US-10-449-902-45993	Sequence 45993, A
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1023	75	4.2	290	7	US-11-191-244-2	Sequence 2, Appli	1096	74	4.1	711	7	US-11-434-137-9166	Sequence 9166, Ap
1024	75	4.2	324	7	US-11-056-355B-22273	Sequence 22273, A	1097	74	4.1	711	7	US-11-434-184-9166	Sequence 9166, Ap
1025	75	4.2	332	7	US-11-388-304-18	Sequence 18, Appli	1098	74	4.1	711	7	US-11-434-199-9166	Sequence 9166, Ap
1026	75	4.2	382	7	US-11-347-740-55	Sequence 55, Appli	1099	74	4.1	711	7	US-11-434-203-9166	Sequence 9166, Ap
1027	75	4.2	402	7	US-11-056-355B-22272	Sequence 22272, A	1100	74	4.1	729	7	US-11-434-137-520	Sequence 520, App
1028	75	4.2	415	7	US-11-056-355B-22271	Sequence 22271, A	1101	74	4.1	729	7	US-11-434-184-520	Sequence 520, App
1029	75	4.2	464	7	US-11-375-221-102	Sequence 102, App	1102	74	4.1	729	7	US-11-434-203-520	Sequence 520, App
1030	75	4.2	486	7	US-11-056-355B-90992	Sequence 90992, A	1103	74	4.1	729	7	US-11-434-203-520	Sequence 520, App
1031	75	4.2	486	7	US-11-056-355B-94748	Sequence 94748, A	1105	74	4.1	964	6	US-10-142-275B-2	Sequence 2, Appli
1032	75	4.2	546	7	US-11-056-355B-79415	Sequence 79415, A	1106	74	4.1	986	7	US-11-226-554-101	Sequence 101, App
1033	75	4.2	550	7	US-11-056-355B-79414	Sequence 79414, A	1107	74	4.1	986	7	US-11-248-718-101	Sequence 101, App
1034	75	4.2	611	7	US-11-330-403-17228	Sequence 17228, A	1108	74	4.1	987	7	US-11-259-133-26	Sequence 26, Appli
1035	75	4.2	722	7	US-11-302-357-10	Sequence 10, Appli	1109	74	4.1	987	7	US-11-226-554-100	Sequence 100, App
1036	75	4.2	971	7	US-11-330-403-7439	Sequence 7439, Ap	1110	74	4.1	987	7	US-11-248-718-100	Sequence 100, App
1037	75	4.2	979	7	US-11-434-137-8936	Sequence 8936, Ap	1111	74	4.1	987	7	US-11-365-989-166	Sequence 166, App
1038	75	4.2	979	7	US-11-434-184-8936	Sequence 8936, Ap	1112	74	4.1	1055	7	US-11-259-133-24	Sequence 24, Appli
1039	75	4.2	979	7	US-11-434-199-8936	Sequence 8936, Ap	1113	74	4.1	1055	7	US-10-511-302A-8	Sequence 8, Appli
1040	75	4.2	979	7	US-11-434-203-8936	Sequence 8936, Ap	1114	74	4.1	1186	6	US-10-511-302A-8	Sequence 8, Appli
1041	75	4.2	991	7	US-11-434-137-6010	Sequence 6010, Ap	1115	73.5	4.1	107	7	US-11-219-563-48	Sequence 6, Appli
1042	75	4.2	991	7	US-11-434-184-6010	Sequence 6010, Ap	1116	73.5	4.1	128	7	US-11-321-444-6	Sequence 217, App
1043	75	4.2	991	7	US-11-434-199-6010	Sequence 6010, Ap	1117	73.5	4.1	221	7	US-11-118-112A-217	Sequence 217, App
1044	75	4.2	991	7	US-11-434-203-6010	Sequence 6010, Ap	1118	73.5	4.1	227	7	US-11-058-952-40	Sequence 40, Appli
1045	75	4.2	1237	7	US-11-293-697-3795	Sequence 3795, Ap	1119	73.5	4.1	232	7	US-11-373-546-8	Sequence 8, Appli
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1048	74.5	4.1	214	7	US-11-297-117-3	Sequence 3, Appli	1122	73.5	4.1	238	7	US-11-434-137-7132	Sequence 7132, Ap
1049	74.5	4.1	235	6	US-10-539-402-24	Sequence 24, Appli	1123	73.5	4.1	238	7	US-11-434-184-7132	Sequence 7132, Ap
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1053	74.5	4.1	392	7	US-11-192-046-40	Sequence 40, Appli	1127	73.5	4.1	246	6	US-10-953-349-1828	Sequence 1828, Ap
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1060	74.5	4.1	432	7	US-11-434-203-8540	Sequence 8540, Ap	1134	73.5	4.1	272	6	US-10-449-903-45962	Sequence 45962, A
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1137	73.5	4.1	284	7	US-11-056-355B-88907	Sequence 88907, A	1211	73	4.0	470	6	US-10-449-902-54114	Sequence 54114, A
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1146	73.5	4.1	320	7	US-11-056-355B-112226	Sequence 112226, A	1220	73	4.0	544	7	US-11-257-579-3	Sequence 3, Appli
1147	73.5	4.1	326	7	US-11-256-332-252	Sequence 252, App	1221	73	4.0	592	6	US-10-539-228-813	Sequence 813, App
1149	73.5	4.1	335	7	US-11-101-316-46	Sequence 46, Appl	1222	73	4.0	592	6	US-10-669-920-838	Sequence 838, App
1150	73.5	4.1	335	7	US-11-376-673-46	Sequence 46, Appl	1223	73	4.0	608	7	US-11-056-355B-50031	Sequence 50031, A
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1152	73.5	4.1	400	7	US-11-174-307B-3776	Sequence 3776, Ap	1225	73	4.0	636	7	US-11-056-355B-50030	Sequence 50030, A
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1156	73.5	4.1	451	7	US-11-429-792-2	Sequence 2, Appli	1229	73	4.0	685	7	US-11-387-672-4	Sequence 4, Appli
1157	73.5	4.1	451	7	US-11-429-793-2	Sequence 2, Appli	1230	73	4.0	884	6	US-10-449-902-56575	Sequence 56575, A
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1165	73.5	4.1	889	7	US-11-338-847-348	Sequence 348, App	1238	73	4.0	147	7	US-11-301-373-59	Sequence 59, Appl
1166	73.5	4.1	894	7	US-11-338-847-337	Sequence 337, App	1239	73	4.0	221	7	US-11-118-112A-96	Sequence 96, Appl
1167	73.5	4.1	895	7	US-11-338-847-347	Sequence 347, App	1240	73	4.0	221	7	US-11-118-112A-98	Sequence 98, Appl
1168	73.5	4.1	900	7	US-11-338-847-333	Sequence 333, App	1241	73	4.0	227	7	US-11-058-952-33	Sequence 33, Appl
1169	73.5	4.1	900	7	US-11-338-847-334	Sequence 334, App	1242	73	4.0	233	6	US-10-511-937-2416	Sequence 2416, Ap
1170	73.5	4.1	1135	6	US-10-449-902-41414	Sequence 41414, A	1243	73	4.0	235	7	US-11-375-221-32	Sequence 32, Appl
1171	73.5	4.1	1176	6	US-11-105-233-63	Sequence 63, Appl	1244	73	4.0	252	7	US-11-337-300-256	Sequence 256, App
1172	73.5	4.1	1398	6	US-10-449-902-41334	Sequence 41334, A	1245	73	4.0	252	7	US-11-024-877-1	Sequence 1, Appli
1173	73.5	4.1	1500	6	US-10-511-756-6	Sequence 6, Appli	1246	73	4.0	314	6	US-10-538-001-119	Sequence 119, App
1174	73.5	4.1	1500	7	US-11-389-432-23	Sequence 23, Appl	1247	73	4.0	327	7	US-11-369-229-6	Sequence 6, Appli
1175	73	4.0	64	7	US-11-229-770-948	Sequence 948, App	1248	73	4.0	327	7	US-11-167-767-42	Sequence 42, Appl
1176	73	4.0	78	7	US-11-287-573-53	Sequence 53, Appl	1249	73	4.0	343	7	US-11-056-355B-69691	Sequence 69691, A
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1180	73	4.0	204	6	US-10-449-902-42626	Sequence 42626, A	1253	73	4.0	461	7	US-11-375-221-54	Sequence 54, Appl
1181	73	4.0	208	7	US-11-265-762-96	Sequence 96, Appl	1254	73	4.0	461	7	US-11-375-221-78	Sequence 78, Appl
1182	73	4.0	208	7	US-11-265-762-110	Sequence 110, App	1255	73	4.0	461	7	US-11-375-221-82	Sequence 82, Appl
1183	73	4.0	218	7	US-11-256-060-18	Sequence 18, Appl	1256	73	4.0	472	6	US-10-538-001-117	Sequence 117, App
1184	73	4.0	231	7	US-11-056-355B-98827	Sequence 98827, A	1257	73	4.0	496	7	US-11-043-842-246	Sequence 246, App
1185	73	4.0	231	7	US-11-056-355B-110066	Sequence 110066, A	1258	73	4.0	511	7	US-11-056-355B-12274	Sequence 12274, A
1186	73	4.0	243	7	US-11-154-103-19	Sequence 19, Appl	1259	73	4.0	528	6	US-10-538-001-118	Sequence 118, App
1187	73	4.0	244	6	US-10-527-100-7	Sequence 7, Appli	1260	73	4.0	558	7	US-11-056-355B-12273	Sequence 12273, A
1188	73	4.0	244	7	US-11-293-697-4183	Sequence 4183, Ap	1261	73	4.0	578	7	US-11-056-355B-12272	Sequence 12272, A
1189	73	4.0	249	6	US-10-553-105-34	Sequence 34, Appl	1262	73	4.0	664	7	US-11-056-355B-47824	Sequence 47824, A
1190	73	4.0	254	6	US-10-553-105-27	Sequence 27, Appl	1263	73	4.0	668	7	US-11-056-355B-47823	Sequence 47823, A
1191	73	4.0	254	7	US-11-118-112A-88	Sequence 88, Appl	1264	73	4.0	679	7	US-11-056-355B-45968	Sequence 45968, A
1192	73	4.0	254	7	US-11-118-112A-90	Sequence 90, Appl	1265	73	4.0	679	7	US-11-056-355B-46061	Sequence 46061, A
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1195	73	4.0	285	7	US-11-056-355B-110065	Sequence 110065, A	1268	73	4.0	680	7	US-11-056-355B-46060	Sequence 46060, A
1196	73	4.0	296	7	US-11-056-355B-98825	Sequence 98825, A	1269	73	4.0	680	7	US-11-056-355B-48050	Sequence 48050, A
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1200	73	4.0	324	7	US-11-056-355B-115847	Sequence 115847, A	1273	73	4.0	878	6	US-10-449-902-46943	Sequence 46943, A
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1202	73	4.0	394	6	US-10-805-394-3504	Sequence 3504, Ap	1275	73	4.0	1450	7	US-11-393-642-4	Sequence 4, Appli
1203	73	4.0	402	7	US-11-056-355B-104607	Sequence 104607, A	1276	73	4.0	1450	7	US-11-393-642-5	Sequence 5, Appli
1204	73	4.0	402	7	US-11-056-355B-115846	Sequence 115846, A	1277	73	4.0	1450	7	US-11-393-642-6	Sequence 6, Appli
1205	73	4.0	415	7	US-11-056-355B-104606	Sequence 104606, A	1278	73	4.0	2434	7	US-11-070-573-48	Sequence 48, Appl
1206	73	4.0	415	7	US-11-056-355B-115845	Sequence 115845, A	1279	73	4.0	4025	6	US-10-553-520-128	Sequence 128, App
1207	73	4.0	458	7	US-11-317-571-93	Sequence 93, Appl	1280	73	4.0	71	7	US-11-412-325-220	Sequence 220, App
1208	73	4.0	458	7	US-11-317-571-120	Sequence 120, App	1281	73	4.0	107	7	US-11-221-902-17	Sequence 17, Appl
1209	73	4.0	465	6	US-10-505-928-549	Sequence 549, App	1282	73	4.0	117	7	US-11-413-563-4	Sequence 4, Appli

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1284	72	4.0	127	7	US-11-291-140-16	Sequence 16, Appl	1357	71.5	4.0	466	7	US-11-375-221-62	Sequence 62, Appl
1285	72	4.0	129	7	US-11-143-737-52	Sequence 52, Appl	1358	71.5	4.0	468	7	US-11-056-355B-83599	Sequence 83599, A
1286	72	4.0	204	6	US-10-449-902-29722	Sequence 29722, A	1359	71.5	4.0	470	7	US-11-293-697-4191	Sequence 4191, Ap
1287	72	4.0	204	6	US-10-449-902-32372	Sequence 32372, A	1360	71.5	4.0	471	7	US-11-056-355B-60132	Sequence 60132, A
1288	72	4.0	220	7	US-11-118-112A-58	Sequence 58, Appl	1361	71.5	4.0	481	7	US-11-056-355B-62018	Sequence 62018, A
1289	72	4.0	245	6	US-10-539-402-34	Sequence 34, Appl	1362	71.5	4.0	495	7	US-11-293-697-4085	Sequence 4085, Ap
1290	72	4.0	249	7	US-11-337-300-49	Sequence 49, Appl	1363	71.5	4.0	522	6	US-10-449-902-46834	Sequence 46834, A
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1292	72	4.0	253	7	US-11-234-731-602	Sequence 602, App	1365	71.5	4.0	553	7	US-11-165-586-26	Sequence 26, Appl
1293	72	4.0	262	6	US-10-541-708-22	Sequence 22, Appl	1366	71.5	4.0	577	6	US-10-953-349-29303	Sequence 29303, A
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1297	72	4.0	320	6	US-10-953-349-4079	Sequence 4079, Ap	1370	71.5	4.0	622	6	US-10-953-349-29302	Sequence 29302, A
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1304	72	4.0	429	7	US-11-330-403-17859	Sequence 17859, A	1377	71.5	4.0	716	6	US-10-570-909-32	Sequence 32, Appl
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1312	72	4.0	864	7	US-11-429-276-296	Sequence 296, App	1385	71	3.9	117	7	US-11-413-563-34	Sequence 34, Appl
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1321	72	4.0	2472	7	US-11-070-573-54	Sequence 54, Appl	1394	71	3.9	214	7	US-11-197-665-82	Sequence 82, Appl
1322	72	4.0	2527	7	US-11-070-573-56	Sequence 56, Appl	1395	71	3.9	234	7	US-11-197-665-10	Sequence 10, Appl
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and is derived by analysis of the total score distribution.

SUMMARIES

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3	1268	70.2	345	2 JC4025	opioid-binding cel
4	1266	70.1	345	2 S03199	opioid-binding pro
5	1259	69.7	345	2 JC1239	opioid-binding pro
6	936.5	51.9	338	2 JC5519	50K glycoprotein p
7	931.5	51.6	338	2 JC4776	limbic-system-asso
8	297.5	16.5	332	2 A31923	amalgam protein pr
9	283.5	15.7	725	1 IJMSNL	neural cell adhesi
10	283.5	15.7	1115	1 IJMSNL	neural cell adhesi
11	279.5	15.5	725	2 JE0099	neural cell adhesi
12	278.5	15.5	1091	1 IJCHNL	neural cell adhesi
13	278.5	15.4	4162	2 T42633	connectin/titin -
14	277.5	15.4	858	1 IJKTNC	neural cell adhesi
15	277.5	15.4	1088	1 IJXJNL	neural cell adhesi
16	276	15.3	761	1 IJHUNG	neural cell adhesi
17	275.5	15.3	853	1 IJBONC	neural cell adhesi
18	273.5	15.1	725	2 JE0100	neural cell adhesi
19	272.5	15.1	1323	2 PN0568	connectin 3B - chi
20	270.5	15.0	1092	1 JN0635	neural cell adhesi
21	261.5	14.5	1091	2 S01998	contactin precurs
22	259	14.3	7962	2 I38346	elastic titin - hu
23	254.5	14.1	5175	2 T20992	hypothetical prote
24	254.5	14.1	5198	2 T43290	hemictentin precurs
25	249.5	13.8	1040	2 A49356	transient axonal g
26	246.5	13.6	1018	2 A54744	contactin 1 precur
27	243.5	13.5	1021	2 A57112	contactin precurs
28	243.5	13.5	1036	2 S22383	axonin 1 precursor
29	241.5	13.4	1018	2 JC4211	neural adhesion pr

30	241.5	13.4	1020	2 S05944	neuronal cell surf
31	240	13.3	3707	2 S18252	heparan sulfate pr
32	235	13.0	662	2 T16525	hypothetical prote
33	234.5	13.0	1040	2 A34695	axonal glycoprotei
34	232.5	12.9	2783	2 T34416	hypothetical prote
35	230.5	12.8	868	2 A46512	CD22 homolog/8 lym
36	227.5	12.6	1051	2 A39712	kinase-like protei
37	226	12.5	6642	2 T29757	protein UNC-89 - C
38	225	12.5	4391	2 A38096	perlecan precursor
39	221.5	12.3	862	2 I49583	differentiation an
40	221	12.2	1896	2 T08851	Down syndrome cell
41	220.5	12.2	898	2 A40114	fasciclin II precu
42	219	12.1	1091	2 A58532	glial cell membran
43	218.5	12.1	1612	2 T30805	dutt1 protein - mo
44	215.5	11.9	1239	1 A32579	neuroglial - fruit
45	214.5	11.9	1070	2 JC4593	protein-tyrosine k
46	214.5	11.9	1651	2 T14160	transmembrane rece
47	214	11.8	495	2 T25750	hypothetical prote
48	211.5	11.7	811	2 A41054	fasciclin II, tran
49	211.5	11.7	871	1 I48696	protein-tyrosine k
50	211.5	11.7	873	2 B41054	fasciclin II PI-li
51	211.5	11.7	881	1 I48697	protein-tyrosine k
52	208.5	11.5	1028	2 A53449	plasmacytoma-asso
53	205.5	11.4	1028	2 I58164	BIG-1 protein - ra
54	204	11.3	1443	2 I50600	neogenin - chicken
55	202	11.2	1273	2 T42405	sax-3 protein - Ca
56	201	11.1	946	1 A47299	rox-related recept
57	199	11.0	1241	2 T37190	nephlin - human
58	198	11.0	847	2 JH0371	B-cell adhesion pr
59	197.5	10.9	1447	2 A54100	tumor suppressor p
60	197	10.9	423	2 T29549	hypothetical prote
61	196	10.9	1906	1 S68235	myosin-light-chain
62	195	10.8	1272	2 S26180	neurofascin - chic
63	195	10.8	1375	2 T13822	frazzled gene prot
64	195	10.8	1526	2 T13823	frazzled gene prot
65	194.5	10.8	1277	2 T30532	neural cell adhesi
66	193	10.7	2029	1 TDFFLK	protein-tyrosine-p
67	192.5	10.7	1209	2 T42718	probable neural ce
68	192.5	10.7	1260	1 S05479	neural cell adhesi
69	192.5	10.7	1268	1 A39640	neural cell adhesi
70	192	10.6	1256	2 T03096	neural cell adhesi
71	189.5	10.5	765	2 C42632	cell adhesion mole
72	189.5	10.5	812	2 B42632	cell adhesion mole
73	189.5	10.5	932	2 A42632	cell adhesion mole
74	188.5	10.4	1265	1 A37967	neural cell adhesi
75	187.5	10.4	1259	2 S36126	neural cell adhesi
76	186.5	10.3	1173	2 T25893	hypothetical prote
77	186.5	10.3	1240	2 T03097	CD0 protein - huma
78	185.5	10.3	404	1 I61596	advanced glycosyla
79	185.5	10.3	702	2 A36319	carcinoembryonic a
80	185	10.3	1344	2 T14316	rig-1 protein - mo
81	185	10.2	1427	2 I51669	tumor suppressor -
82	184	10.2	582	1 BNRT3	myelin-associated
83	184	10.2	626	1 BNRT3	myelin-associated
84	184	10.2	1033	2 S19247	neural cell adhesi
85	183	10.1	1232	2 T43027	neural cell adhesi
86	183	10.1	1328	2 T23007	hypothetical prote
87	182.5	10.1	875	2 T33434	hypothetical prote
88	182.5	10.1	1336	2 I60598	Fit-1 tyrosine kin
89	182	10.1	626	1 A61084	myelin-associated
90	181.5	10.0	1197	2 T30581	neural cell adhesi
91	181.5	10.0	1333	2 T78875	receptor tyrosine
92	179	9.9	637	2 B33785	myelin-associated
93	179	9.9	917	2 I48950	telencephalin prec
94	178.5	9.9	483	2 T17346	hypothetical prote
95	178	9.9	1259	2 A43425	Bravo/Nr-CAM cell
96	177.5	9.8	797	2 S38579	fibroblast growth
97	177	9.8	1015	2 T32186	hypothetical prote
98	176.5	9.8	772	2 T13078	KIAA0992 protein -
99	176	9.7	964	2 T15746	hypothetical prote
100	174	9.6	3375	2 T19821	hypothetical prote
101	174	9.6	6658	2 T13931	projectin - fruit
102	174	9.6	26926	1 I38344	titin, cardiac mus

103	173.5	9.6	1021	2	T42634	connectin/titin -	176	151	8.4	976	1	TVMSMD	macrophage colony-
104	172.5	9.6	264	2	T26976	hypothetical prote	177	151	8.4	1287	2	T30988	hypothetical prote
105	172.5	9.6	976	2	T29583	hypothetical prote	178	150.5	8.3	349	2	A34815	carcinoembryonic a
106	172.5	9.6	1880	2	T18531	tractin - medicina	179	150.5	8.3	824	2	S24108	protein-tyrosine k
107	172	9.5	286	2	A28333	carcinoembryonic a	180	150.5	8.3	1298	2	A48999	protein-tyrosine k
108	172	9.5	647	2	A35648	B-cell adhesion pr	181	150	8.3	769	2	S16236	fibroblast growth
109	171.5	9.5	1338	2	S09982	protein-tyrosine k	182	150	8.3	822	2	A45081	fibroblast growth
110	171	9.5	464	2	C30127	transmembrane carc	183	150	8.3	822	2	A41794	keratinocyte growt
111	171	9.5	526	1	A32164	bilialy glycoprote	184	149.5	8.3	739	2	JS0675	vascular cell adhe
112	171	9.5	1257	1	A41060	neural cell adhesi	185	149.5	8.3	1501	2	S18148	protein-tyrosine-p
113	170	9.4	812	1	A36477	fibroblast growth	186	149.5	8.3	1863	2	S46217	pregnancy-specific
114	169	9.4	764	2	A49448	irregular chiasm C	187	149	8.3	335	2	H43354	protein-tyrosine-p
115	169	9.4	814	1	A39752	fibroblast growth	188	149	8.3	1894	2	C54689	DM-GRASP precursor
116	168	9.3	1330	2	S49010	embryonic receptor	189	148.5	8.2	587	2	JH0464	adhesion molecule
117	168	9.3	2051	2	T30938	receptor tyrosine	190	148.5	8.2	588	2	JH0506	protein-tyrosine-p
118	168	9.3	2295	2	C88369	protein unc-52 (im	191	148.5	8.2	1907	2	S08893	protein-tyrosine-k
119	167.5	9.3	523	2	S10478	neurolin - goldfis	192	147.5	8.2	876	2	I49152	protein-tyrosine-p
120	167.5	9.3	1694	2	S50065	sialoadhesin - mou	193	147.5	8.2	1499	2	I50212	protein-tyrosine-p
121	167	9.2	816	2	A49151	fibroblast growth	194	147	8.1	402	2	T09062	probable advanced
122	167	9.2	822	1	TVMSFG	fibroblast growth	195	147	8.1	406	2	E43354	pregnancy-specific
123	167	9.2	1356	2	JCL1402	protein-tyrosine k	196	146.5	8.1	773	2	T46283	hypothetical prote
124	165.5	9.2	538	2	JC2457	vascular cell adhe	197	146	8.1	428	2	A27658	pregnancy-specific
125	165.5	9.2	646	2	I38049	cell surface glyco	198	146	8.1	852	2	I51259	tyrosine kinase C
126	165	9.1	584	2	T08678	hypothetical prote	199	146	8.1	1088	1	PPRTGA	platelet-derived g
127	165	9.1	822	2	I49289	fibroblast growth	200	146	8.1	1089	1	S33727	platelet-derived g
128	165	9.1	822	2	S29840	fibroblast growth	201	145.5	8.1	739	2	JN0581	vascular cell adhe
129	165	9.1	2222	2	T13924	sedk protein - fru	202	145.5	8.1	799	2	S18209	fibroblast growth
130	164.5	9.1	583	2	I39428	alcam - human	203	145.5	8.1	1898	2	S46216	leukocyte antigen-
131	164.5	9.1	832	2	JH0393	fibroblast growth	204	145	8.0	972	1	TVHUMD	macrophage colony-
132	164	9.1	628	2	I38000	Lutheran blood gro	205	144.5	8.0	1262	1	B48758	protein-tyrosine-p
133	163	9.0	818	2	T19120	hypothetical prote	206	144.5	8.0	1496	1	A48758	protein-tyrosine-p
134	162.5	9.0	1535	2	S46224	peroxidasin - fru	207	143.5	7.9	1177	2	T18594	hypothetical prote
135	162	9.0	321	2	JH0395	bilialy glycoprote	208	143.5	7.9	13055	2	T16580	hypothetical prote
136	162	9.0	351	2	JH0396	bilialy glycoprote	209	143	7.9	620	2	JH0593	Schwann cell myel
137	162	9.0	417	2	JH0394	bilialy glycoprote	210	143	7.9	687	2	A49636	soluble vascular e
138	161	8.9	588	2	I37202	B-CAM protein - hu	211	143	7.9	1011	2	T13669	neuromusculin - fr
139	161	8.9	2541	2	T29340	hypothetical prote	212	142.5	7.9	326	2	F43354	pregnancy-specific
140	160.5	8.9	980	1	TVCNMD	macrophage colony-	213	142.5	7.9	435	2	D33258	pregnancy-specific
141	160	8.9	662	2	C40862	heparin-binding gr	214	142.5	7.9	739	2	A41288	vascular cell adhe
142	160	8.9	822	1	TVHURG	fibroblast growth	215	142	7.9	806	2	A35963	protein-tyrosine k
143	160	8.9	1437	2	T31093	probable protein-t	216	141.5	7.8	324	2	G43354	pregnancy-specific
144	160	8.9	6831	2	A88852	protein unc-22 (im	217	141.5	7.8	333	2	A43354	pregnancy-specific
145	160	8.9	6839	2	S57242	twitchin (similari	218	141.5	7.8	789	2	T28714	hypothetical prote
146	158.5	8.8	1199	2	TN0030	hypothetical prote	219	141.5	7.8	1227	2	T23004	hypothetical prote
147	158	8.7	361	2	PN0020	fibroblast growth	220	141.5	7.8	1355	2	T28715	hypothetical prote
148	158	8.7	822	2	B54846	fibroblast growth	221	141	7.8	254	2	C42691	fibroblast growth
149	157.5	8.7	941	1	TVMVD	protein-tyrosine k	222	141	7.8	821	1	TVHUF2	fibroblast growth
150	157	8.7	299	2	S56749	junctional adhesio	223	140.5	7.8	397	2	C43354	pregnancy-specific
151	156.5	8.7	416	1	A42879	advanced glycosyla	224	140.5	7.8	705	2	S51635	fibroblast growth
152	156	8.6	978	2	S16385	macrophage colony-	225	140.5	7.8	823	2	B35963	protein-tyrosine k
153	156	8.6	7160	2	T27935	hypothetical prote	226	140.5	7.8	1089	1	PFHUGA	platelet-derived g
154	155.5	8.6	880	2	B53743	protein-tyrosine k	227	140	7.8	800	1	TVHUF2	fibroblast growth
155	155.5	8.6	1138	2	S24614	myosin-binding pro	228	140	7.8	800	2	A48991	heparin-binding gr
156	155	8.6	458	1	WMMSR1	bilialy glycoprote	229	140	7.8	801	2	I55363	fibroblast growth
157	155	8.6	458	2	JCL1509	bilialy glycoprote	230	140	7.8	890	1	A53743	protein-tyrosine k
158	155	8.6	521	2	JCL1508	bilialy glycoprote	231	140	7.8	976	1	TVHUKT	protein-tyrosine k
159	155	8.6	521	2	S34338	bilialy glycoprote	232	139.5	7.7	395	2	D43354	pregnancy-specific
160	155	8.6	1363	2	I58375	protein-tyrosine k	233	139.5	7.7	417	2	A28277	pregnancy-specific
161	155	8.6	1367	2	A41288	protein-tyrosine k	234	139.5	7.7	419	2	A33258	pregnancy-specific
162	154.5	8.6	602	2	A45769	acetylcholine rece	235	139.5	7.7	419	2	A31135	pregnancy-specific
163	154.5	8.6	1897	1	TDHULK	leukocyte antigen-	236	139.5	7.7	426	2	A35964	pregnancy-specific
164	154	8.5	1348	2	S51656	vascular endotheli	237	139.5	7.7	821	1	TVMSBK	fibroblast growth
165	153.5	8.5	588	2	A45254	surface glycoprote	238	139.5	7.7	1052	2	B49120	protein-tyrosine k
166	153	8.5	1912	2	A56178	protein-tyrosine-p	239	139	7.7	824	2	S36439	protein C18F3.2 [1
167	152.5	8.4	267	2	A38449	probable tumor sup	240	139	7.7	987	2	A88746	hypothetical prote
168	152.5	8.4	458	2	S23969	cell-adhesion mole	241	139	7.7	3488	2	T34418	hemolin - cecropia
169	152	8.4	525	1	A58674	neurotrophin-3 rec	242	138.5	7.7	413	2	S65948	pregnancy-specific
170	152	8.4	803	1	S35695	neurotrophin-3 rec	243	138.5	7.7	426	2	B33258	pregnancy-specific
171	152	8.4	819	1	TVCHFG	fibroblast growth	244	138.5	7.7	426	2	A35341	platelet-derived g
172	152	8.4	880	1	JC4166	protein-tyrosine k	245	138	7.6	1087	2	I51552	pregnancy-specific
173	152	8.4	1123	2	S36846	myosin-binding pro	246	137.5	7.6	419	2	B54312	platelet-specific
174	151.5	8.4	344	2	A27691	nonspecific cross-	247	137.5	7.6	882	2	I38912	receptor tyrosine
175	151.5	8.4	422	2	S32357	glial growth facto	248	137.5	7.6	1379	2	JC4954	vascular endotheli

249 137 7.6 282 2 C28928 pregnancy-specific
 250 137 7.6 424 2 B36109 pregnancy-specific
 251 137 7.6 458 2 S68177 C-CAM2a protein is
 252 137 7.6 519 2 A44783 ecto-ATPase precu
 253 137 7.6 524 2 A35341 kettin - fruit fly
 254 136.5 7.6 738 2 A40096 platelet-endotheli
 255 136.5 7.6 822 2 S19947 fibroblast growth
 256 135.5 7.5 822 2 B49151 fibroblast growth
 257 135.5 7.5 975 2 T30816 macrophage colony-
 258 134.5 7.4 419 2 JC4123 pregnancy-specific
 259 134.5 7.4 428 2 I57486 pregnancy-specific
 260 134.5 7.4 480 2 JS0032 pregnancy-specific
 261 134.5 7.4 482 2 A56182 fibroblast growth
 262 134.5 7.4 647 2 B41288 vascular cell adhe
 263 134.5 7.4 729 2 A49120 fibroblast growth
 264 134 7.4 238 2 T22098 hypothetical prote
 265 134 7.4 424 2 A34595 pregnancy-specific
 266 134 7.4 1147 2 A59307 myosin-light-chain
 267 133.5 7.4 888 2 S23065 ufo protein - mous
 268 133 7.4 336 2 C27658 pregnancy-specific
 269 133 7.4 413 2 A37778 hemolin precursor
 270 133 7.4 473 2 D88976 protein F54E2.4 [i
 271 133 7.4 612 2 I73633 gene trkC protein
 272 133 7.4 818 2 JC4058 fibroblast growth
 273 133 7.4 825 2 A55178 neurotrophin recep
 274 133 7.4 839 1 I73632 neurotrophin-3 rec
 275 132.5 7.3 273 2 B28928 pregnancy-specific
 276 132.5 7.3 275 2 A28928 pregnancy-specific
 277 132.5 7.3 584 2 I50419 s-glycerin precurs
 278 132.5 7.3 856 2 I58411 protein-tyrosine k
 279 132 7.3 1048 2 T30815 platelet-derived g
 280 131.5 7.3 480 2 B56182 fibroblast growth
 281 131.5 7.3 307 2 A38429 keratinocyte growt
 282 131 7.3 499 2 S33766 platelet-derived g
 283 131 7.3 811 2 PN0689 connectin 1 - chic
 284 131 7.3 1106 1 PHUGB platelet-derived g
 285 130.5 7.2 310 2 JL0119 Fc gamma (IgG) rec
 286 130.5 7.2 323 2 S06946 Fc gamma (IgG) rec
 287 130 7.2 802 1 TVHUF4 fibroblast growth
 288 129.5 7.2 419 2 A36109 pregnancy-specific
 289 129.5 7.2 707 2 A54846 fibroblast growth
 290 129.5 7.2 1040 2 A57638 receptor tyrosine
 291 129.5 7.2 1103 2 T22889 hypothetical prote
 292 129 7.1 392 1 RWHUPD poliovirus recepto
 293 129 7.1 417 1 RWHUPA poliovirus recepto
 294 129 7.1 1098 1 PFSNRB platelet-derived g
 295 128.5 7.1 682 2 A35969 heparin-binding gr
 296 128 7.1 806 1 TVHUF3 fibroblast growth
 297 127.5 7.1 241 2 S32359 glial growth facto
 298 127 7.0 992 2 A39331 protein-tyrosine k
 299 126.5 7.0 592 2 S25705 Ig mu chain - shee
 300 126.5 7.0 790 2 A39627 protein-tyrosine k
 301 126 7.0 477 1 I73631 brain-derived neur
 302 126 7.0 822 1 A56853 brain-derived neur
 303 126 7.0 940 2 A40985 projectin - fruit
 304 126 7.0 1000 2 S18827 Flt3 protein - mou
 305 125.5 6.9 251 2 T15495 hypothetical prote
 306 125.5 6.9 278 2 JC1507 biliary glycoprote
 307 125.5 6.9 335 2 B33251 nonspecific cross-
 308 125.5 6.9 341 2 JC1511 biliary glycoprote
 309 125.5 6.9 518 2 JC4024 poliovirus recepto
 310 125.5 6.9 526 2 S70587 butyrophilin precu
 311 125.5 6.9 975 1 TVNSKT protein-tyrosine k
 312 125 6.9 278 2 JC1506 biliary glycoprote
 313 125 6.9 341 2 JC1512 biliary glycoprote
 314 125 6.9 977 2 I45877 protein-tyrosine k
 315 124.5 6.9 750 2 S41051 fibroblast growth
 316 124.5 6.9 829 2 JC4583 fibroblast growth
 317 124.5 6.9 960 1 JN0677 protein-tyrosine k
 318 124 6.9 428 2 A39037 carcinoembryonic a
 319 124 6.9 426 2 C55181 pregnancy-specific
 320 124 6.9 426 2 S09016 pregnancy-specific
 321 124 6.9 426 2 B35334 pregnancy-specific

322 124 436 2 B55181 pregnancy-specific
 323 124 495 2 A55181 pregnancy-specific
 324 124 6.9 650 1 JC1450 fibroblast growth
 325 124 6.9 999 2 I38547 novel cellular pro
 326 124 6.9 1666 2 A48594 skelemin - mouse
 327 123.5 6.8 402 2 A54312 pregnancy-specific
 328 123.5 6.8 640 2 A43273 heregulin precurs
 329 123 6.8 351 2 B34595 heregulin-specific
 330 123 6.8 476 1 A35104 brain-derived neur
 331 123 6.8 821 1 S06943 myosin-light-chain
 332 123 6.8 1176 2 JN0583 neu differentiation
 333 122.5 6.8 230 2 A56210 heregulin precurs
 334 122.5 6.8 241 2 A43273 heregulin precurs
 335 122.5 6.8 462 2 I38404 neu differentiation
 336 122.5 6.8 636 2 I61718 neu differentiation
 337 122.5 6.8 637 2 C43273 heregulin precurs
 338 122.5 6.8 639 2 C43273 heregulin precurs
 339 122.5 6.8 645 2 B43273 heregulin, splice
 340 122.5 6.8 662 2 I61722 neu differentiation
 341 122 6.8 272 2 I48268 biliary glycoprote
 342 122 6.8 850 2 JC5700 ErbB kinase activa
 343 121.5 6.7 332 2 JN0067 pregnancy-specific
 344 121.5 6.7 365 2 JC7780 coxsackie- and ade
 345 121.5 6.7 474 1 C39667 brain-derived neur
 346 121.5 6.7 476 1 B39667 brain-derived neur
 347 121.5 6.7 520 1 S44099 brain-derived neur
 348 121.5 6.7 818 1 S44098 brain-derived neur
 349 121.5 6.7 821 1 A39667 brain-derived neur
 350 121.5 6.7 1450 2 A44027 16SK myofibrillar
 351 121 6.7 292 2 T44044 glycoprotein limpo
 352 121 6.7 733 2 I49293 fibroblast growth
 353 121 6.7 994 2 I49276 c-mex tyrosine kin
 354 121 6.7 1142 2 S36845 myosin-binding pro
 355 120.5 6.7 212 2 C33258 pregnancy-specific
 356 120.5 6.7 353 2 S51242 heparin-binding fi
 357 120.5 6.7 742 2 S24600 projectin - fruit
 358 120 6.6 729 2 A56795 fibroblast growth
 359 119.5 6.6 684 2 S60266 novel antigen rece
 360 119.5 6.6 6805 2 S20901 titin - rabbit (fr
 361 119 6.6 707 2 JC7763 neuronal leucine-r
 362 119 6.6 820 2 S17295 fibroblast growth
 363 119 6.6 860 2 JC5702 ErbB kinase activa
 364 119 6.6 868 2 JC5701 ErbB kinase activa
 365 119 6.6 1274 2 S55050 cardiac myosin-bin
 366 118 6.5 1451 2 S42167 190K protein - hum
 367 117.5 6.5 182 2 I83053 pregnancy-specific
 368 117.5 6.5 335 2 A35514 pregnancy-specific
 369 117.5 6.5 569 2 A36187 interleukin-1 rece
 370 117.5 6.5 978 1 A49814 protein-tyrosine k
 371 117 6.5 621 2 B57431 myosin-binding C-p
 372 117 6.5 825 1 A40026 neurotrophin-3 rec
 373 117 6.5 894 1 A41527 protein-tyrosine k
 374 116.5 6.5 243 2 A37982 calcium vector pro
 375 116.5 6.5 282 2 T17219 hypothetical prote
 376 116.5 6.5 317 2 JL0118 Fc gamma (IgG) rec
 377 116.5 6.5 599 2 T16774 hypothetical prote
 378 116 6.4 253 2 T15475 hypothetical prote
 379 116 6.4 268 2 T23555 hypothetical prote
 380 116 6.4 330 2 I46691 CDB6 precursor - r
 381 116 6.4 416 2 A54017 colon carcinoma-as
 382 116 6.4 993 2 A36873 protein-tyrosine k
 383 115.5 6.4 526 2 A37821 butyrophilin - bov
 384 115.5 6.4 942 2 S23251 protein-tyrosine k
 385 115 6.4 166 2 A33402 pregnancy-specific
 386 115 6.4 813 1 A49123 fibroblast growth
 387 115 6.4 1462 1 B36182 protein-tyrosine-p
 388 114.5 6.3 326 2 JC4124 pregnancy-specific
 389 114 6.3 302 2 C36464 fibroblast growth
 390 114 6.3 432 1 RWMQ74 T-cell surface gly
 391 114 6.3 713 2 I50128 fibroblast growth
 392 114 6.3 947 1 B44294 unc-5 protein, lon
 393 114 6.3 1132 2 A35089 myosin-binding pro
 394 113.5 6.3 344 2 A41357 Fc gamma (IgG) rec

395	113.5	6.3	374	1	A39878	Fc gamma (IgG) rec	468	100	5.5	395	2	T05906	probable polygalac
396	113.5	6.3	547	1	S28904	intercellular adhe	469	100	5.5	531	2	S06016	intercellular adhe
397	113.5	6.3	1465	2	A53329	165K protein, skel	470	100	5.5	537	2	I49769	intercellular adhe
398	113	6.3	530	2	A53329	poliovirus recepto	471	100	5.5	641	2	D71170	hypothetical prote
399	112.5	6.2	304	1	RWCHH7	cell surface glyco	472	99	5.5	537	2	A45815	intercellular adhe
400	112.5	6.2	503	2	JC5287	SHP substrate-1 pr	473	99	5.5	869	2	T44440	chitinase (EC 3.2.
401	112.5	6.2	666	2	H89581	protein dim-1 [imp	474	99	5.5	1160	2	F88369	protein unc-52 [im
402	112.5	6.2	954	2	I51703	c-kit-related kina	475	98.5	5.5	629	2	A46500	ly-9.2 antigen - m
403	112.5	6.2	2109	2	E89066	protein H05009.1 [476	98	5.4	238	2	A49633	Ig lambda-like cha
404	112.5	6.2	2109	2	T33247	hypothetical prote	477	98	5.4	524	2	JQ0683	type-specific anti
405	112	6.2	573	2	S12838	Ig mu chain precu	478	98	5.4	544	2	JC5018	intercellular adhe
406	112	6.2	1327	2	T09402	immunoglobulin-lik	479	98	5.4	773	1	QRRBG	secretory componen
407	111.5	6.2	335	2	C54312	pregnancy-specific	480	98	5.4	1000	2	I46521	titin - rabbit (fr
408	111.5	6.2	392	2	B44194	poliovirus recepto	481	97.5	5.4	197	2	PQ0327	heparin-binding fi
409	111.5	6.2	417	2	A44194	poliovirus recepto	482	97.5	5.4	270	2	S65739	basigin precursor
410	111.5	6.2	567	2	S29498	lymphocyte antigen	483	97	5.4	172	2	B26414	95K nonspecific cr
411	111	6.1	210	2	JC4122	pregnancy-specific	484	97	5.4	465	2	B27235	deacetylase/diipe
412	111	6.1	292	2	T44230	hypothetical prote	485	97	5.4	874	2	T92548	hypothetical prote
413	111	6.1	398	2	S17428	interleukin-1 rece	486	96.5	5.3	309	2	I49503	B-lymphocyte activ
414	111	6.1	748	2	S41050	fibroblast growth	487	96.5	5.3	364	2	T46926	hypothetical prote
415	110.5	6.1	509	2	JC5288	SHP substrate-1 pr	488	96.5	5.3	437	2	A64488	hypothetical prote
416	110.5	6.1	513	2	JC5289	SHP substrate-1 pr	489	96.5	5.3	475	2	I76668	pregnancy-specific
417	110	6.1	285	2	S36903	Fc gamma (IgG) rec	490	96.5	5.3	580	2	A46538	Ig heavy chain, se
418	110	6.1	508	2	A33378	fasciclin III prec	491	96.5	5.3	709	2	A35364	carcinoembryonic a
419	110	6.1	919	2	T32541	unc-5 protein - Ca	492	96	5.3	455	1	MRMS	Ig mu chain C regi
420	110	6.1	1579	2	E91290	probable invasin [493	96	5.3	455	2	A24976	Ig mu chain C regi
421	110	6.1	1700	2	G86131	probable invasin 2	494	96	5.3	476	1	MHMSM	Ig mu chain C regi
422	109.5	6.1	164	2	T19795	hypothetical prote	495	96	5.3	562	2	G02426	interleukin-1 rece
423	109.5	6.1	196	2	T19794	hypothetical prote	496	96	5.3	790	1	TVHUTT	nerve growth facto
424	109.5	6.1	206	2	A40305	biliary glycoprote	497	95.5	5.3	309	2	S15674	cell surface glyco
425	109.5	6.1	470	2	S22080	Ig heavy chain pre	498	95.5	5.3	330	2	A29915	teratocarcinoma gl
426	109.5	6.1	532	1	A29849	intercellular adhe	499	95.5	5.3	345	2	A46052	vascular cell adhe
427	108	6.0	207	2	A56190	titin - rat (fragm	500	95.5	5.3	375	2	I60125	PDGF receptor beta
428	108	6.0	267	2	I72882	Fc gamma receptor	501	95	5.3	267	2	A35902	Fc gamma (IgG) rec
429	108	6.0	467	1	HLMSP3	poliovirus recepto	502	95	5.3	277	2	I52825	gene MAC25 protein
430	108	6.0	474	1	OMHUIB	alpha-1-B-glycopro	503	95	5.3	329	2	S50031	prostacyclin-stimu
431	107.5	6.0	352	2	I77374	pregnancy-specific	504	95	5.3	329	2	A44065	fibroblast growth
432	107.5	6.0	404	2	A46480	Fc gamma (IgG) rec	505	95	5.3	799	1	TVRRTB	nerve growth facto
433	107.5	6.0	537	2	A46611	myosin-binding pro	506	95	5.3	383	2	AC1018	large repetitive p
434	106.5	5.9	336	2	A42632	Fit-1S protein pre	507	94.5	5.2	182	2	A34647	pregnancy-specific
435	106.5	5.9	367	1	MHCH	Ig mu chain C regi	508	94.5	5.2	355	2	D72174	D9R protein - vari
436	106	5.9	407	2	T07332	hypothetical prote	509	94.5	5.2	1184	2	T09484	cartilage intermed
437	105.5	5.8	326	2	T37450	interleukin-1 beta	510	94.5	5.2	1280	2	AB1981	hypothetical prote
438	105.5	5.8	487	2	T28804	hypothetical prote	511	94.5	5.2	1452	1	S17670	protein-tyrosine-p
439	105	5.8	131	2	T20334	hypothetical prote	512	94.5	5.2	2347	1	TVHURS	kinase-related pro
440	105	5.8	269	2	A46506	leukocyte activati	513	94	5.2	328	2	I47159	Ig gamma 2a chain
441	104.5	5.8	290	2	F42527	Bl6R protein - vac	514	94	5.2	757	2	I45956	polymeric immunogl
442	104	5.8	1471	2	T19506	hypothetical prote	515	93.5	5.2	194	2	T29925	hypothetical prote
443	103.5	5.7	240	2	JC4121	pregnancy-specific	516	93.5	5.2	265	2	A55811	carcinoembryonic a
444	103.5	5.7	326	1	MWVZ15	Bl5R protein precu	517	93.5	5.2	354	2	T46877	B20R protein - var
445	103.5	5.7	445	2	S65133	butyrophilin - mou	518	93.5	5.2	354	2	T28616	hypothetical prote
446	103.5	5.7	531	2	S20900	titin - mouse (fra	519	93.5	5.2	1366	2	B84924	hypothetical prote
447	103.5	5.7	538	2	I68093	PRR2 delta - human	520	93	5.1	144	2	B40098	colorectal cancer
448	103	5.7	618	2	T08685	hypothetical prote	521	93	5.1	267	2	I56110	Fc-gamma RIIB-alp
449	103	5.7	943	2	B45082	neutrophilic recep	522	93	5.1	299	2	I46690	CD80 precursor - r
450	102.5	5.7	257	2	S00682	IgG Fc receptor al	523	93	5.1	352	2	T32433	hypothetical prote
451	102.5	5.7	336	2	I48471	Fc gamma (IgG) rec	524	93	5.1	352	2	S16844	titin - rabbit (fr
452	102.5	5.7	1021	2	T39207	leukocyte surface	525	92.5	5.1	213	2	JE0247	Ig lambda chain NI
453	102	5.6	351	1	SAV2VW	surface antigen pr	526	92.5	5.1	274	2	T32736	hypothetical prote
454	102	5.6	478	2	I53960	PRR2 alpha - human	527	92.5	5.1	298	2	H64247	translation elonga
455	102	5.6	1398	2	T25668	hypothetical prote	528	92.5	5.1	590	2	I56526	interleukin 1 rece
456	101.5	5.6	275	2	JC7604	CD86 spliced varia	529	92.5	5.1	1220	2	T32916	hypothetical prote
457	101.5	5.6	329	1	A48754	B7-2 antigen - hum	530	92	5.1	328	2	I47160	Ig gamma 2b chain
458	101.5	5.6	625	2	T16777	hypothetical prote	531	92	5.1	460	2	JC2194	vasoactive intesti
459	101.5	5.6	937	2	A45082	neutrophilic recep	532	92	5.1	545	2	JU0341	intercellular adhe
460	101	5.6	351	1	SAV2WR	surface antigen pr	533	91.5	5.1	455	2	H96797	hypothetical prote
461	101	5.6	353	1	SAV2VC	surface antigen pr	534	91	5.0	132	2	S14077	Ig kappa chain - A
462	101	5.6	421	2	T46266	hypothetical prote	535	91	5.0	370	2	A96741	hypothetical prote
463	101	5.6	458	1	RWH074	T-cell surface gly	536	91	5.0	416	2	S33473	interleukin-1 rece
464	101	5.6	751	2	I48748	semaphorin E - mou	537	91	5.0	427	2	G02034	killer cell inhibi
465	100.5	5.6	274	2	A47639	OX-2 membrane glyc	538	90.5	5.0	391	2	T09058	butyrophilin homol
466	100	5.5	235	2	S20000	Ig light chain pre	539	90.5	5.0	1269	2	F90538	hypothetical prote
467	100	5.5	304	2	B88746	protein C18F3.3 [i	540	90	5.0	283	1	FCMSG1	Fc gamma (IgG) rec

541	90	5.0	296	2	I46021	Fc-gamma receptor	614	85	4.7	1526	2	T19473	hypothetical prote
542	90	5.0	432	1	RWC274	T-cell surface gly	615	85	4.7	2274	2	T30258	adenomatous polyo
543	90	5.0	444	2	G01924	KIR (cl-2) NK rece	616	85	4.7	2339	2	S41121	acetyl-CoA carboxy
544	90	5.0	576	2	A32604	interleukin-1 rece	617	85	4.7	4351	2	T00252	MSGFI protein - ra
545	90	5.0	721	2	C82939	virulence associat	618	84.5	4.7	240	2	S01299	OX-45 membrane gly
546	90	5.0	858	1	VCLJG2	env polyprotein pr	619	84.5	4.7	243	2	A53244	leukocyte antigen
547	90	5.0	1357	2	T29265	hypothetical protei	620	84.5	4.7	330	2	A40071	Fc gamma (IGG) rec
548	90	5.0	2282	2	T42717	DNA-binding protei	621	84.5	4.7	330	2	I49660	FC gamma -1/gamma-2
549	89.5	5.0	131	2	F45893	T-cell receptor al	622	84.5	4.7	385	2	T01332	hypothetical prote
550	89.5	5.0	245	2	A30154	IGF receptor alpha	623	84.5	4.7	466	2	AF0172	asparagine-tRNA li
551	89.5	5.0	254	1	JU0107	FC gamma (IGC) rec	624	84.5	4.7	727	2	S54512	hypothetical prote
552	89.5	5.0	362	2	A56745	microfibril-associ	625	84.5	4.7	897	2	B65127	Probable bifunctio
553	89.5	5.0	1134	1	JN0711	protein-tyrosine k	626	84.5	4.7	1133	2	T01757	hypothetical prote
554	89.5	5.0	1691	1	D54609	protein-tyrosine-p	627	84.5	4.7	1227	2	T48028	hypothetical prote
555	89	4.9	257	2	P50401	basigin type II -	628	84	4.7	1136	1	KVMS21	IG kappa chain pre
556	89	4.9	271	2	S43512	GP42/basigin prote	629	84	4.7	162	2	I51668	tumor suppressor -
557	89	4.9	273	2	JX0107	basigin precursor	630	84	4.7	225	2	G89936	conserved hypothet
558	89	4.9	275	2	P50402	basigin type III -	631	84	4.7	240	2	JL0143	antigen BCM1 precu
559	89	4.9	429	1	EHRT	IG epsilon chain C	632	84	4.7	246	2	A29523	T-cell surface gly
560	89	4.9	598	2	A57249	beta-galactosidase	633	84	4.7	337	2	AG0963	hypothetical prote
561	89	4.9	769	1	Q8RTGS	secretory componen	634	84	4.7	466	2	JC5897	Killer cell inhibi
562	89	4.9	1452	1	S17659	protein-tyrosine-p	635	84	4.7	495	2	JC2195	vasoactive intesti
563	88.5	4.9	309	2	I49522	Gene B7-2 protein	636	84	4.7	737	2	I39547	S-protein secretio
564	88	4.9	331	2	T15587	hypothetical prote	637	84	4.7	997	2	D75012	hypothetical prote
565	88	4.9	757	1	S48841	secretory componen	638	84	4.7	1442	2	S72441	protein-tyrosine-p
566	88	4.9	832	2	AD1086	internalin protein	639	84	4.7	1477	2	B43855	high-molecular-wei
567	88	4.9	4436	2	E71086	hypothetical prote	640	84	4.7	1536	2	A43855	high-molecular-wei
568	87.5	4.8	151	2	T31607	hypothetical prote	641	83.5	4.6	110	2	B30583	T-cell receptor de
569	87.5	4.8	280	2	I55577	FC gamma (IGC) rec	642	83.5	4.6	134	2	S21917	IG kappa chain V r
570	87.5	4.8	321	2	I54766	B-lymphocyte activ	643	83.5	4.6	245	2	T07071	beta-fructofuranos
571	87.5	4.8	368	2	S17980	pgal protein - Asp	644	83.5	4.6	315	1	HNV24X	hemagglutinin prec
572	87.5	4.8	402	2	T29703	hypothetical prote	645	83.5	4.6	328	2	S30444	ST2 protein - huma
573	87.5	4.8	660	2	H71376	probable tpr prote	646	83.5	4.6	374	2	S69339	IG heavy chain V r
574	87	4.8	359	2	A37115	undecaprenyl-PP-Mu	647	83.5	4.6	405	1	B42806	Cytochrome P450 CV
575	87	4.8	383	2	T21946	hypothetical prote	648	83.5	4.6	490	2	B96952	sucrase-6-phosphat
576	87	4.8	477	2	B64115	asparagine-tRNA li	649	83.5	4.6	513	2	F86320	hypothetical prote
577	87	4.8	814	2	I40048	S-layer protein pr	650	83.5	4.6	583	2	S57721	csfB protein - Clo
578	87	4.8	974	1	A49714	protein-tyrosine k	651	83.5	4.6	1054	2	T18304	acid trehalase hom
579	87	4.8	2458	2	T17420	probable polyketid	652	83.5	4.6	1657	2	T25421	hypothetical prote
580	86.5	4.8	235	2	S25058	IG kappa chain - m	653	83	4.6	220	2	A49444	IG gamma-1 heavy c
581	86.5	4.8	278	1	TDRTOX	OX-2 membrane gly	654	83	4.6	313	2	JQ1862	3IR protein - vari
582	86.5	4.8	440	2	D71175	hypothetical prote	655	83	4.6	315	1	HNV2VW	hemagglutinin prec
583	86.5	4.8	1533	2	T00344	hypothetical prote	656	83	4.6	410	2	C69197	ATP-dependent 26S
584	86	4.8	387	2	T04320	polygalacturonase	657	83	4.6	555	2	JQ1526	interleukin-1 rece
585	86	4.8	387	2	T07591	polygalacturonase	658	83	4.6	563	2	C95874	conserved hypotet
586	86	4.8	444	2	G01925	KIR (cl-11) NK rec	659	83	4.6	633	2	AE2312	transketolase (imp
587	86	4.8	501	1	A60005	glycoprotein A pre	660	83	4.6	680	2	JC5895	DNA-binding protei
588	86	4.8	501	1	VBEBWA	glycoprotein A pre	661	83	4.6	767	2	S41479	hypothetical prote
589	86	4.8	501	1	VBEBWA	glycoprotein A pre	662	83	4.6	1014	2	T24412	hypothetical prote
590	86	4.8	505	1	VBEBWH	glycoprotein gp57-	663	83	4.6	1033	2	A12359	hypothetical prote
591	86	4.8	580	2	A36683	hypothetical prote	664	83	4.6	2638	1	A42545	genome polyprotein
592	86	4.8	587	2	S36231	beta-fructofuranos	665	83	4.6	4836	2	T14346	herc2 protein - mo
593	86	4.8	856	1	A44963	env polyprotein pr	666	82.5	4.6	125	2	A53627	fibroblast growth
594	86	4.8	1394	2	S60762	IGA-specific serin	667	82.5	4.6	160	2	I47163	cytolytic trigger
595	86	4.8	1711	2	AB1283	peptidoglycan link	668	82.5	4.6	197	2	T25933	IG kappa chain (WM
596	85.5	4.7	475	2	A54879	pregnancy-specific	669	82.5	4.6	233	2	JC5322	p53 specific singl
597	85.5	4.7	510	2	PC4054	cardiac C-protein	670	82.5	4.6	247	1	PMWST2	T-cell surface gly
598	85.5	4.7	593	1	DTCHPH	purH bifunctional	671	82.5	4.6	315	2	T37438	hemagglutinin - va
599	85.5	4.7	764	1	QRHUS	secretory componen	672	82.5	4.6	429	2	T36088	probable secreted
600	85.5	4.7	1145	1	GNLJEV	HIV-1 retropepsin	673	82.5	4.6	433	2	S31436	IG upsilon chain -
601	85.5	4.7	1146	1	GNLJ22	HIV-1 retropepsin	674	82.5	4.6	610	2	T25262	hypothetical prote
602	85.5	4.7	1146	1	GNLJEW	HIV-1 retropepsin	675	82.5	4.6	871	2	H81430	translation initia
603	85.5	4.7	1732	2	T30836	lysine-specific cy	676	82.5	4.6	1553	2	T18502	hypothetical prote
604	85	4.7	505	2	B84831	hypothetical prote	677	82	4.5	120	2	D29775	IG kappa chain pre
605	85	4.7	635	2	JC5896	Killer cell inhibi	678	82	4.5	225	2	I51335	IG lambda chain -
606	85	4.7	753	2	B36268	platelet glycoprot	679	82	4.5	230	2	S49449	IG lambda chain -
607	85	4.7	778	2	A60798	platelet glycoprot	680	82	4.5	270	2	A34636	FC-gamma receptor
608	85	4.7	788	2	A26547	platelet glycoprot	681	82	4.5	288	2	A45803	B-cell-restricted
609	85	4.7	788	2	I77349	platelet glycoprot	682	82	4.5	313	2	H36854	hemagglutinin - va
610	85	4.7	817	2	A48721	titin, muscle - ch	683	82	4.5	318	2	F72171	K9R protein - vari
611	85	4.7	832	2	E71492	hypothetical prote	684	82	4.5	489	1	VBETA	glycoprotein A - t
612	85	4.7	939	2	I41197	eeae protein (enter	685	82	4.5	523	1	A60408	glycoprotein gp57-
613	85	4.7	1436	2	JC5290	protein-tyrosine-p	686	82	4.5	630	2	T38637	hypothetical prote

687	82	4.5	663	1	ORECIC	colicin I receptor	760	79.5	4.4	290	2	C97533	pyruvate dehydroge
688	82	4.5	820	2	Tl4879	hypothetical prote	761	79.5	4.4	306	2	AE2752	pyruvate dehydroge
689	82	4.5	841	2	JC5894	Killer cell inhibi	762	79.5	4.4	468	1	A41242	interleukin-6 rece
690	82	4.5	842	2	T04555	hypothetical prote	763	79.5	4.4	474	2	I50830	Ig mu chain - Lepi
691	82	4.5	1125	1	S57846	protein-tyrosine k	764	79.5	4.4	522	2	B42804	immunodominant typ
692	82	4.5	1222	2	T22490	hypothetical prote	765	79.5	4.4	558	2	A44964	apical membrane an
693	82	4.5	1577	2	T30858	glucosyltransferas	766	79.5	4.4	653	2	A49722	endoglin precursor
694	81.5	4.5	107	2	PL0268	Ig kappa chain v r	767	79.5	4.4	766	1	CDHU26	dipeptidyl-peptida
695	81.5	4.5	240	2	A41797	Ig light chain - s	768	79.5	4.4	1022	1	S00503	Na+/K+-exchanging
696	81.5	4.5	247	2	J43954	T-cell surface gly	769	79.5	4.4	1034	1	A53663	enteropeptidase (E
697	81.5	4.5	259	2	JC7109	ST2V protein - hum	770	79.5	4.4	1036	2	B69368	hypothetical prote
698	81.5	4.5	656	2	T23338	hypothetical prote	771	79.5	4.4	1156	2	T23308	hypothetical prote
699	81.5	4.5	1183	2	A89135	protein F25G6.2 [i	772	79.5	4.4	1185	2	A42404	collagen adhesin -
700	81.5	4.5	1203	2	S27545	pullulanase - ther	773	79.5	4.4	1409	2	T42522	protein-tyrosine-p
701	81.5	4.5	1336	2	T17479	hypothetical prote	774	79.5	4.4	1422	2	T30111	hypothetical prote
702	81.5	4.5	1983	2	G86643	hypothetical prote	775	79	4.4	91	2	SL7638	Ig kappa chain v r
703	81	4.5	234	2	A52317	Ig kappa chain pre	776	79	4.4	101	2	H37262	Ig heavy chain v r
704	81	4.5	247	2	A55717	myelin/oligodendro	777	79	4.4	231	2	S25753	Ig lambda chain -
705	81	4.5	314	1	HNW2VW	hemagglutinin prec	778	79	4.4	348	2	C81284	cystathionine beta
706	81	4.5	314	1	JQ1793	hemagglutinin prec	779	79	4.4	370	2	G97001	endoglucanase fami
707	81	4.5	451	2	S71754	cellular hepatitis	780	79	4.4	387	2	T04322	polygalacturonase
708	81	4.5	545	2	A38447	oligopeptide ABC t	781	79	4.4	403	2	T20727	hypothetical prote
709	81	4.5	568	2	A45804	Ig mu chain C regi	782	79	4.4	432	2	S30193	T-cell surface gly
710	81	4.5	571	2	H69584	acetolactate synth	783	79	4.4	450	2	B97292	probable ATP-depen
711	81	4.5	578	2	B96583	hypothetical prote	784	79	4.4	474	1	G2MS11	Ig gamma-2b chain
712	81	4.5	585	2	A46507	Ig alpha chain - c	785	79	4.4	659	2	G91009	colicin I receptor
713	81	4.5	588	2	C83836	subtilisin-type pr	786	79	4.4	753	2	G02173	semaphorin III fam
714	81	4.5	637	2	B83052	DnaK protein PA476	787	79	4.4	807	2	A71663	DNA gyrase chain B
715	81	4.5	665	2	E86775	ribonuclease (impo	788	79	4.4	875	2	H90371	proteinase [import
716	80.5	4.5	248	1	Q0B841	probable glycoprot	789	79	4.4	1175	2	D85089	hypothetical prote
717	80.5	4.5	269	2	B97501	hypothetical prote	790	79	4.4	1204	2	C75015	probable pyrolysin
718	80.5	4.5	273	2	G89856	conserved hypochet	791	79	4.4	1350	2	AF2005	RNA polymerase bet
719	80.5	4.5	277	2	I47162	Ig gamma 4 chain c	792	79	4.4	1439	2	T27110	hypothetical prote
720	80.5	4.5	298	2	T30086	hypothetical prote	793	78.5	4.3	111	2	D37266	Ig kappa chain v r
721	80.5	4.5	327	2	B97076	UDP-glucose 4-epim	794	78.5	4.3	115	2	B46518	Ig l1 chain v regi
722	80.5	4.5	358	2	A99214	sUA5 related conse	795	78.5	4.3	140	2	PH1498	Ig heavy chain v r
723	80.5	4.5	459	2	A46254	CD4 precursor - ra	796	78.5	4.3	228	2	S29575	Ig light chain - r
724	80.5	4.5	466	2	AF0616	asparagine-tRNA li	797	78.5	4.3	290	1	XYRBM	arylamine N-acetyl
725	80.5	4.5	517	2	B87644	4-coumarate-CoA li	798	78.5	4.3	323	2	JC2578	DNA repair protein
726	80.5	4.5	554	2	A91250	probable portal Al	799	78.5	4.3	373	2	JH0155	pectin lyase (EC 4
727	80.5	4.5	596	2	D84972	ABC transporter At	800	78.5	4.3	392	2	T03229	enoyl-facyl-carrie
728	80.5	4.5	613	2	T41565	hypothetical prote	801	78.5	4.3	434	2	D88305	protein R03D7.4 [i
729	80.5	4.5	881	2	S67026	probable membrane	802	78.5	4.3	434	2	D88305	transcription elon
730	80.5	4.5	1025	2	G81722	polymorphic membra	803	78.5	4.3	553	1	SMEBH1	flagellar hook-ass
731	80.5	4.5	1128	1	T08312	plasmid replicatio	804	78.5	4.3	553	2	AH0640	flagellar hook-ass
732	80.5	4.5	1349	2	S51471	killer toxin insen	805	78.5	4.3	556	2	A44441	B-cell antigen CD1
733	80.5	4.5	1375	2	JT0345	dextranucrase (EC	806	78.5	4.3	561	2	T45607	hypothetical prote
734	80.5	4.5	1433	2	T30261	chitinase (EC 3.2.	807	78.5	4.3	590	2	A56535	gadd34 protein - l
735	80.5	4.5	1457	1	A48066	protein-tyrosine-p	808	78.5	4.3	592	2	S54489	phosphoribosylamin
736	80.5	4.5	1538	2	E70874	probable ppsB prot	809	78.5	4.3	605	1	A48665	methylmalonyl-CoA
737	80.5	4.5	4588	2	T28667	dynein beta heavy	810	78.5	4.3	668	2	JQ0773	penicillin-binding
738	80	4.4	104	2	JH0345	T-cell receptor al	811	78.5	4.3	682	2	S46417	heat shock protein
739	80	4.4	150	2	A40862	fibroblast growth -	812	78.5	4.3	693	2	B90520	ABC transporter at
740	80	4.4	233	2	I51383	Ig lambda chain -	813	78.5	4.3	759	2	AG3402	polyposphate kina
741	80	4.4	239	2	G02630	PcalpharB - human	814	78.5	4.3	829	2	E87305	TonB-dependent rec
742	80	4.4	287	2	JH0332	IgA (Fc) receptor,	815	78.5	4.3	934	2	B29838	parasporel crystal
743	80	4.4	313	2	T28598	hypothetical prote	816	78.5	4.3	1019	2	T40813	probable cell divi
744	80	4.4	425	2	JE0086	SH3-domain binding	817	78.5	4.3	1070	2	T34385	hypothetical prote
745	80	4.4	433	1	S48515	adenylosuccinica s	818	78.5	4.3	1217	2	T00270	hypothetical prote
746	80	4.4	454	1	MHHY	Ig mu chain C regi	819	78.5	4.3	1252	2	T31119	mshQ protein - Vib
747	80	4.4	466	2	H96991	secreted protein c	820	78.5	4.3	1385	2	A88554	protein C38C10.5a
748	80	4.4	552	2	S42253	probable N1L prote	821	78.5	4.3	1391	2	B88554	protein C38C10.5b
749	80	4.4	642	2	S44542	probable membrane	822	78.5	4.3	1440	2	JC8312	protein-tyrosine-p
750	80	4.4	680	2	PN0510	integrin beta-3 ch	823	78.5	4.3	1687	2	T43144	vitellogenin li pr
751	80	4.4	937	2	T04194	hypothetical prote	824	78.5	4.3	5188	2	B85547	probable RXR famil
752	80	4.4	995	2	A56599	embryo kinase 5 -	825	78.5	4.3	5291	2	F90696	hypothetical prote
753	80	4.4	1200	2	T48194	hypothetical prote	826	78	4.3	1325	2	S62676	herregulin isoform
754	80	4.4	3343	2	T42207	breast cancer susc	827	78	4.3	1351	2	PT0178	Ig kappa chain pre
755	79.5	4.4	155	2	A41675	telokin - rabbit	828	78	4.3	132	2	A55410	Ig light chain v r
756	79.5	4.4	204	2	A69197	hypothetical prote	829	78	4.3	137	2	C45893	T-cell receptor al
757	79.5	4.4	220	2	I55963	Lyt-2.1 lymphocyte	830	78	4.3	178	2	G71195	hypothetical prote
758	79.5	4.4	250	2	A34342	IgG Fc receptor al	831	78	4.3	233	2	S29577	Ig light chain - r
759	79.5	4.4	261	2	S29360	FC gamma (IgG) rec	832	78	4.3	255	2	JC7593	SH2 domain-contain

833	78	4.3	301	1	G64491	thioedoxin-disulf	906	76.5	4.2	267	1	RWMS08	T-cell receptor al
834	78	4.3	320	1	I47158	Ig gamma 1 chain c	907	76.5	4.2	299	1	AHRB	Ig alpha chain C r
835	78	4.3	370	1	HLHUA3	MHC Class I histoc	908	76.5	4.2	305	2	B75129	thiamin biosynthes
836	78	4.3	413	2	AG3267	amino-acid N-acety	909	76.5	4.2	332	2	D83745	3-oxoacyl-lacyl-ca
837	78	4.3	460	2	S67174	hypothetical prote	910	76.5	4.2	403	2	S53477	IMP dehydrogenase
838	78	4.3	475	2	T44566	conserved hypotet	911	76.5	4.2	428	2	AH3536	dihydroliipoamide s
839	78	4.3	481	2	E82217	asparaginyl-tRNA s	912	76.5	4.2	431	2	A86601	hypothetical prote
840	78	4.3	542	2	A84554	hypothetical prote	913	76.5	4.2	431	2	G72022	probable sodium-tr
841	78	4.3	702	2	T21148	hypothetical prote	914	76.5	4.2	457	2	A27449	T-cell surface gly
842	78	4.3	872	2	C84513	Mutator-like trans	915	76.5	4.2	463	2	T14884	hypothetical prote
843	78	4.3	980	2	H90681	probable flagellin	916	76.5	4.2	483	2	A69745	hypothetical prote
844	78	4.3	980	2	H85532	probable structura	917	76.5	4.2	515	2	H86202	hypothetical prote
845	78	4.3	1016	2	H71460	probable outer mem	918	76.5	4.2	516	2	E70035	levanase homolog y
846	78	4.3	1029	2	F96602	hypothetical prote	919	76.5	4.2	528	2	PC4025	intercellular adhe
847	78	4.3	1138	1	S24065	protein-tyrosine k	920	76.5	4.2	547	2	S75904	hypothetical prote
848	78	4.3	1217	2	F97177	alpha-glucosidase	921	76.5	4.2	563	2	T20631	hypothetical prote
849	78	4.3	2185	1	GNNYSV	genome polyprotein	922	76.5	4.2	572	1	HNNZB3	hemagglutinin-neur
850	78	4.3	2256	2	AD1018	large repetitive p	923	76.5	4.2	573	2	F89719	protein F09B12.1 [
851	78	4.3	4302	2	A38971	polycystic kidney	924	76.5	4.2	573	2	T20632	hypothetical prote
852	77.5	4.3	119	2	PH1519	Ig heavy chain v r	925	76.5	4.2	622	2	A36915	fructanase - Bacte
853	77.5	4.3	140	2	A36194	Ig heavy chain v r	926	76.5	4.2	653	2	B30908	probable host spec
854	77.5	4.3	284	2	S75817	hypothetical prote	927	76.5	4.2	656	2	B71290	conserved hypotet
855	77.5	4.3	307	2	C71002	hypothetical prote	928	76.5	4.2	740	2	AD0485	probable exported
856	77.5	4.3	309	2	T15747	hypothetical prote	929	76.5	4.2	749	2	E86774	hypothetical prote
857	77.5	4.3	315	1	HNZVT	hemagglutinin prec	930	76.5	4.2	775	2	G90996	probable host spec
858	77.5	4.3	428	2	T48167	hypothetical prote	931	76.5	4.2	782	2	A85693	hypothetical prote
859	77.5	4.3	446	2	S40295	Ig gamma-2a chain	932	76.5	4.2	896	2	T22081	valyl-tRNA synthet
860	77.5	4.3	466	2	C85619	asparagine tRNA sy	933	76.5	4.2	913	2	E75554	protein F2 - Strep
861	77.5	4.3	466	2	E90755	asparagine tRNA sy	934	76.5	4.2	1039	2	T30856	protein-tyrosine k
862	77.5	4.3	469	1	T7HUE2	transcription fact	935	76.5	4.2	1124	1	I58388	hypothetical prote
863	77.5	4.3	532	2	C42804	immunodominant typ	936	76.5	4.2	1131	2	T14517	hypothetical prote
864	77.5	4.3	534	2	S60205	phosphonacetaldeh	937	76.5	4.2	1151	2	S48431	probable membrane
865	77.5	4.3	584	2	F70522	probable polyketid	938	76.5	4.2	1248	2	C89874	autolysin [impor
866	77.5	4.3	593	2	A11235	internalin protein	939	76.5	4.2	1363	2	C84346	hypothetical prote
867	77.5	4.3	655	2	T34219	hypothetical prote	940	76.5	4.2	1377	2	I54632	tsh protein - Esch
868	77.5	4.3	668	2	S49639	probable membrane	941	76.5	4.2	1648	2	S61654	probable membrane
869	77.5	4.3	676	2	T30480	envelope protein h	942	76.5	4.2	2477	2	S14428	fibronectin precu
870	77.5	4.3	852	1	VCLJGG	env polyprotein pr	943	76	4.2	91	2	PH1071	Ig light chain v r
871	77.5	4.3	888	2	A54280	cell differentiat	944	76	4.2	107	2	PD0011	Ig kappa chain v r
872	77.5	4.3	1192	2	T08609	hypothetical prote	945	76	4.2	108	2	G30560	Ig kappa chain v r
873	77.5	4.3	1474	2	F69009	probable membrane	946	76	4.2	108	2	S38720	Ig light chain v r
874	77.5	4.3	1515	2	A40203	4-alpha-glucanotra	947	76	4.2	118	2	I33932	Ig kappa chain pre
875	77.5	4.3	1819	2	D97033	uncharacterized pr	948	76	4.2	120	2	C29775	Ig kappa chain pre
876	77.5	4.3	1825	2	C88400	protein H19M22.1 [949	76	4.2	161	2	S04931	T-cell receptor de
877	77.5	4.3	1825	2	T32828	hypothetical prote	950	76	4.2	251	2	S64927	probable membrane
878	77.5	4.3	3329	2	T42205	breast cancer susc	951	76	4.2	254	2	B75052	coenzyme pqq synth
879	77.5	4.3	3329	2	T30904	breast cancer tumo	952	76	4.2	310	2	F90011	conserved hypotet
880	77.5	4.3	3591	1	S21010	filamentous hemagg	953	76	4.2	327	2	T07104	2'-hydroxydihydro
881	77	4.3	107	2	PC4405	Ig kappa chain v r	954	76	4.2	327	2	S06611	Ig gamma-2 chain C
882	77	4.3	128	2	S40343	Ig kappa chain v-J	955	76	4.2	365	2	D87526	hypothetical prote
883	77	4.3	234	2	S01320	Ig kappa chain pre	956	76	4.2	426	2	H84846	probable polygalac
884	77	4.3	302	2	S05079	hypothetical prote	957	76	4.2	430	2	T28143	tapasin 1 homolog,
885	77	4.3	328	2	I47161	Ig gamma 3 chain c	958	76	4.2	431	2	F71476	probable sodium-tr
886	77	4.3	338	2	S09276	Ig alpha chain C r	959	76	4.2	450	1	MHDG	Ig mu chain C regi
887	77	4.3	384	2	E84871	probable polygalac	960	76	4.2	473	2	H83676	pyruvate dehydroge
888	77	4.3	439	2	A81251	probable peptidogl	961	76	4.2	501	2	E96509	protein P27F5.17 [
889	77	4.3	614	2	A88466	protein B0244.2 li	962	76	4.2	506	1	ACRYG1	nicotinic acetylch
890	77	4.3	817	2	F86742	ribonuclease [limpo	963	76	4.2	511	2	B4685	probable seed stor
891	77	4.3	859	2	AC2089	adenylate cyclase	964	76	4.2	516	2	A44494	CAMP-responsive el
892	77	4.3	879	2	C90879	hypothetical prote	965	76	4.2	577	2	T48530	clathrin binding p
893	77	4.3	879	2	G85739	hypothetical prote	966	76	4.2	656	2	AC0429	2',3'-cyclic-nucle
894	77	4.3	928	2	A87749	protein F55C7.7c. [967	76	4.2	859	1	VCLJCT	env polyprotein pr
895	77	4.3	976	2	C96958	ACT domain contain	968	76	4.2	1020	2	A46405	C protein alpha an
896	77	4.3	1071	1	PXBHYA	H+-exporting ATPas	969	76	4.2	1151	2	S03722	DNA-directed DNA p
897	77	4.3	1176	2	A33856	surface-layer 125k	970	76	4.2	1196	2	H86389	hypothetical prote
898	77	4.3	2488	2	T42739	guanine nucleotide	971	76	4.2	1278	2	A47462	probable DNA-direc
899	77	4.3	3562	2	A47171	chondroitin sulfat	972	76	4.2	1366	2	S57664	IgA-specific metal
900	76.5	4.2	135	2	PH1492	Ig heavy chain v r	973	76	4.2	2380	2	T29551	hypothetical prote
901	76.5	4.2	136	2	A49137	Ig kappa chain pre	974	75.5	4.2	104	2	JC6076	anti-D-dimer monoc
902	76.5	4.2	178	2	S29594	Ig gamma chain (WM	975	75.5	4.2	114	2	S44119	Ig kappa chain v-J
903	76.5	4.2	232	2	S17399	Ig lambda chain pr	976	75.5	4.2	123	2	S35479	Ig kappa chain pre
904	76.5	4.2	236	2	A24637	T-cell surface gly	977	75.5	4.2	131	2	S09259	Ig kappa chain pre
905	76.5	4.2	252	2	AF2719	arginine-tRNA-prot	978	75.5	4.2	131	2	D29380	Ig kappa chain pre

979	75.5	4.2	132	2	PH0106	anti-digoxin trans	1052	75	4.2	1311	2	T33757	hypothetical prote
980	75.5	4.2	133	2	S40324	Ig kappa chain v r	1053	75	4.2	1313	2	G82887	hypothetical prote
981	75.5	4.2	140	1	HVMSG7	Ig heavy chain pre	1054	75	4.2	1476	2	AC2220	hypothetical prote
982	75.5	4.2	140	2	PH1489	Ig heavy chain v r	1055	75	4.2	1661	2	H71439	hypothetical prote
983	75.5	4.2	189	2	T39849	anaphase promoting	1056	75	4.2	1672	2	T46237	hypothetical prote
984	75.5	4.2	231	2	PC4155	Ig gamma-2b chain	1057	75	4.2	2291	2	S11238	polymerase - Berne
985	75.5	4.2	234	2	A39356	Ig lambda chain pr	1058	75	4.2	2413	2	S34670	splicing factor PR
986	75.5	4.2	248	2	F96855	hypothetical prote	1059	75	4.2	2500	2	G71609	hypothetical prote
987	75.5	4.2	249	2	C69081	acetyl-CoA synthet	1060	74.5	4.1	116	1	HVMS1B	Ig heavy chain pre
988	75.5	4.2	262	2	T42986	v-cyclin - ateline	1061	74.5	4.1	119	2	PH1517	Ig heavy chain v r
989	75.5	4.2	316	2	F86157	hypothetical prote	1062	74.5	4.1	119	2	PH1516	Ig heavy chain v r
990	75.5	4.2	341	2	S72445	DNA-binding protei	1063	74.5	4.1	140	2	PH1488	Ig heavy chain v r
991	75.5	4.2	362	2	S16303	polygalacturonase	1064	74.5	4.1	192	2	T02893	hypothetical prote
992	75.5	4.2	398	2	T46475	hypothetical prote	1065	74.5	4.1	232	2	S25756	Ig lambda chain -
993	75.5	4.2	402	2	F70850	DNA-directed DNA p	1066	74.5	4.1	243	2	AC3071	transcription regu
994	75.5	4.2	504	2	S00390	Ig gamma chain (cl	1067	74.5	4.1	277	2	S29922	Salu8L protein pre
995	75.5	4.2	524	2	D87440	2-isopropylmalate	1068	74.5	4.1	370	1	HVRKCS	Ig mu chain C regi
996	75.5	4.2	569	2	A46462	T cell activation	1069	74.5	4.1	397	2	S70987	dnaN protein - Myc
997	75.5	4.2	580	2	S49308	beta-fructofuranos	1070	74.5	4.1	438	2	B97712	hypothetical prote
998	75.5	4.2	582	2	S53814	DEAD box protein -	1071	74.5	4.1	466	1	SYSCNT	L2 protein - human
999	75.5	4.2	641	2	JC7142	dextranase (EC 3.2	1072	74.5	4.1	468	1	P2WL51	hypothetical prote
1000	75.5	4.2	691	1	S46735	NADPH-ferrihemopro	1073	74.5	4.1	501	2	S74341	Ig heavy chain pre
1001	75.5	4.2	710	1	A46273	mitochondrial inte	1074	74.5	4.1	549	2	S04845	Ig heavy chain pre
1002	75.5	4.2	713	1	ALBSG7	cyclomaltodextrin	1075	74.5	4.1	591	1	CBBY2	L-lactate dehydrog
1003	75.5	4.2	739	2	A55314	glycine-tRNA ligas	1076	74.5	4.1	644	2	S50552	hypothetical prote
1004	75.5	4.2	746	2	E64701	conserved hypotet	1077	74.5	4.1	663	2	AG0782	colicin I receptor
1005	75.5	4.2	771	2	B70564	hypothetical prote	1078	74.5	4.1	693	2	JN0843	heat shock protein
1006	75.5	4.2	815	2	AB2444	hypothetical prote	1079	74.5	4.1	729	2	T46270	hypothetical prote
1007	75.5	4.2	857	1	S05943	gelation factor -	1080	74.5	4.1	807	2	T39479	histone transcript
1008	75.5	4.2	918	2	D71407	hypothetical prote	1081	74.5	4.1	862	2	E88594	protein Y48A6B.11
1009	75.5	4.2	1068	2	S73091	hypothetical prote	1082	74.5	4.1	899	2	A83019	conserved hypotet
1010	75.5	4.2	1787	2	A99273	hypothetical prote	1083	74.5	4.1	947	2	T26314	hypothetical prote
1011	75.5	4.2	1818	2	AE3011	conserved hypotet	1084	74.5	4.1	1043	2	D84900	hypothetical prote
1012	75.5	4.2	1871	2	D96658	probable DNA polym	1085	74.5	4.1	1183	2	S63046	probable translati
1013	75.5	4.2	1894	2	T02155	DNA-directed DNA p	1086	74.5	4.1	1403	2	T11583	hypothetical prote
1014	75.5	4.2	2065	1	FNBO	fibronectin - bovi	1087	74.5	4.1	1622	2	T45240	microtubule-associ
1015	75.5	4.2	2205	2	F82884	hypothetical prote	1088	74.5	4.1	1825	2	S13507	microtubule-associ
1016	75.5	4.2	6669	2	S55034	nebulin, skeletal	1089	74.5	4.1	1830	2	A37981	kinase-related pro
1017	75	4.2	106	2	A49138	IgA kappa rheumato	1090	74.5	4.1	2338	2	I73957	toxin B - Clostrid
1018	75.5	4.2	115	2	B26524	T-cell receptor be	1091	74.5	4.1	2366	2	S10317	hypothetical prote
1019	75.5	4.2	117	2	S40362	Ig kappa chain - h	1092	74.5	4.1	2761	2	T21064	hypothetical prote
1020	75.5	4.2	128	2	A47159	Ig lambda chain v r	1093	74.5	4.1	4572	2	S57908	hypothetical 527K
1021	75	4.2	130	2	C29380	Ig kappa chain pre	1094	74.5	4.1	4639	1	A54794	dyein heavy chain
1022	75	4.2	131	2	D34904	Ig kappa chain pre	1095	74	4.1	107	2	S12954	Ig kappa chain v r
1023	75	4.2	148	2	PH0115	Ig heavy chain pre	1096	74	4.1	108	2	T26681	hypothetical prote
1024	75	4.2	157	2	D31327	IgE receptor alpha	1097	74	4.1	131	2	S52449	Ig kappa chain v r
1025	75	4.2	215	2	A57843	sodium channel bet	1098	74	4.1	196	2	S72716	4-coumarate-CoA li
1026	75	4.2	246	2	E69230	hypothetical prote	1099	74	4.1	221	1	Q0BE48	BARF1 protein - hu
1027	75	4.2	268	2	A56446	Ig heavy chain v r	1100	74	4.1	231	2	S25751	Ig lambda chain -
1028	75	4.2	283	2	AH1767	protoporphyrinogen	1101	74	4.1	248	2	B45831	MHC class I histoc
1029	75	4.2	285	2	B82842	spermidine synthas	1102	74	4.1	277	2	D42521	A38L protein - vac
1030	75	4.2	297	2	AC2380	hypothetical prote	1103	74	4.1	365	2	I37476	MHC class I histoc
1031	75	4.2	307	1	RWMSRC	T-cell receptor be	1104	74	4.1	365	2	I56039	HLA-A30.3 precurs
1032	75	4.2	321	2	S10006	hypothetical prote	1105	74	4.1	365	2	I38519	MHC class I histoc
1033	75	4.2	359	2	AF3184	beta-lactamase lim	1106	74	4.1	416	1	A41267	transcription fact
1034	75	4.2	364	2	S03535	class I histocompa	1107	74	4.1	429	2	AC1522	flagellar hook-ass
1035	75	4.2	392	2	T34095	zinc finger protei	1108	74	4.1	438	1	HVRKCS	Ig mu chain C regi
1036	75	4.2	393	2	T03216	endo-1,4-beta-gluc	1109	74	4.1	454	1	B64706	hemolysin - Helic
1037	75	4.2	394	2	G69230	hypothetical prote	1110	74	4.1	454	2	T26296	hypothetical prote
1038	75	4.2	416	2	E64140	probable envelope	1111	74	4.1	461	1	HVRKCO	Ig mu chain C regi
1039	75	4.2	435	2	T42613	contains cell adhe	1112	74	4.1	468	1	TVMSK2	transcription fact
1040	75	4.2	439	2	G97159	hypothetical prote	1113	74	4.1	474	2	T47299	hypothetical prote
1041	75	4.2	444	2	B90053	hypothetical prote	1114	74	4.1	514	2	G89903	conserved hypotet
1042	75	4.2	476	2	S64291	glycoprotein F - h	1115	74	4.1	523	2	F85489	2-isopropylmalate
1043	75	4.2	479	1	VGEBE2	hypothetical prote	1116	74	4.1	523	2	F90638	2-isopropylmalate
1044	75	4.2	535	2	S76554	hypothetical prote	1117	74	4.1	523	2	B64729	hypothetical prote
1045	75	4.2	574	2	T29005	hypothetical prote	1118	74	4.1	562	2	AH2084	laccase (EC 1.10.3
1046	75	4.2	577	2	I50731	Ig heavy chain - n	1119	74	4.1	573	2	T02743	probable acyl-CoA
1047	75	4.2	701	2	C97910	ATP-dependent prot	1120	74	4.1	579	2	D87063	hypothetical prote
1048	75	4.2	743	2	T34853	probable fusidic a	1121	74	4.1	587	2	S63033	hypothetical prote
1049	75	4.2	775	1	JQ1639	outer layer protei	1122	74	4.1	701	2	C97302	subtilisin-like pr
1050	75	4.2	780	2	T31548	hypothetical prote	1123	74	4.1	755	2	T48553	WD40-repeat protei
1051	75	4.2	1242	1	DJBEC1	DNA-directed DNA p	1124	74	4.1	876	2	T51507	

1125	74	4.1	879	2	H64888	membrane protein y	1198	73	4.0	469	2	D95989	conserved hypother
1126	74	4.1	908	2	T25035	hypothetical prote	1199	73	4.0	478	2	S47040	gene Tt52 protein
1127	74	4.1	966	2	E87473	TonB-dependent rec	1200	73	4.0	481	2	C97238	ATP dependent RNA
1128	74	4.1	1085	2	JC2227	probable helicase	1201	73	4.0	523	2	A12696	serine proteinase
1129	74	4.1	1128	2	H90538	hypothetical prote	1202	73	4.0	523	2	A97479	probable serine pr
1130	74	4.1	1132	1	Q8BPL	host specificity p	1203	73	4.0	565	2	H69342	GTP-binding protei
1131	74	4.1	1136	1	S57845	protein-tyrosine k	1204	73	4.0	586	2	T45945	laccase-like prote
1132	74	4.1	1137	2	B90734	probable host spec	1205	73	4.0	657	2	AD1525	probable cell surf
1133	74	4.1	1482	2	S13495	pregnancy zone pro	1206	73	4.0	671	2	T23015	hypothetical prote
1134	74	4.1	1488	2	C70984	probable ppsE prot	1207	73	4.0	673	2	H86761	glycine-tRNA ligas
1135	74	4.1	1524	2	A96950	DNA segregation AT	1208	73	4.0	673	2	T41768	ACKNPV orf23 - Bom
1136	74	4.1	1963	2	B98002	IgA-specific metal	1209	73	4.0	688	2	S39491	proteochlorophyllid
1137	74	4.1	2185	1	GNNYSH	genome polyprotein	1210	73	4.0	701	2	H95039	hypothetical prote
1138	74	4.1	2812	2	T43271	phosphotidylinosit	1211	73	4.0	722	2	D70200	polyribonucleotide
1139	73.5	4.1	64	2	S20961	keratinocyte growt	1212	73	4.0	745	2	B33856	hypothetical 80K p
1140	73.5	4.1	96	2	PH1070	Ig light chain V r	1213	73	4.0	754	2	E86592	general secretion
1141	73.5	4.1	97	2	S26341	Ig light chain V r	1214	73	4.0	754	2	D72032	general secretion
1142	73.5	4.1	119	2	PH1510	Ig heavy chain V r	1215	73	4.0	771	2	AF2056	cation transportin
1143	73.5	4.1	119	2	PH1518	Ig heavy chain V r	1216	73	4.0	772	2	A46108	outer capsid prote
1144	73.5	4.1	133	2	PC1155	Ig heavy chain pre	1217	73	4.0	858	2	T12142	lipoxigenase (EC 1
1145	73.5	4.1	144	2	PH1493	Ig heavy chain V r	1218	73	4.0	870	2	T47454	lipoxigenase AtLOX
1146	73.5	4.1	140	2	PH1486	Ig heavy chain V r	1219	73	4.0	896	2	TQ2391	lipoxigenase (EC 1
1147	73.5	4.1	140	2	PH1483	Ig heavy chain V r	1220	73	4.0	897	2	S67283	hypothetical prote
1148	73.5	4.1	229	2	A20969	Ig kappa chain pre	1221	73	4.0	935	2	S66306	hypothetical prote
1149	73.5	4.1	309	2	T09564	glutaminyl-peptide	1222	73	4.0	980	2	T39630	valine-tRNA ligase
1150	73.5	4.1	339	2	T28137	Ig V-region-like B	1223	73	4.0	1095	2	T24061	hypothetical prote
1151	73.5	4.1	340	2	T28137	Ig V-region-like B	1224	73	4.0	1336	2	T18288	hypothetical prote
1152	73.5	4.1	366	2	AF0497	DNA-directed DNA p	1225	73	4.0	1473	2	A35186	ABC transport prot
1153	73.5	4.1	380	2	S12839	Ig heavy chain pre	1226	73	4.0	1518	2	T28880	salivary agglutini
1154	73.5	4.1	388	2	E95007	sugar isomerase do	1227	73	4.0	1815	2	B95942	hypothetical prote
1155	73.5	4.1	400	2	T22853	probable cathepsin	1228	73	4.0	2207	2	S09553	conserved hypother
1156	73.5	4.1	418	2	G87469	ThiJ/PfPI family p	1229	73	4.0	2210	1	RXXPTV	genome polyprotein
1157	73.5	4.1	422	2	A96912	glutamate-1-semial	1230	73	4.0	2907	2	A57278	fibrillin-2 precur
1158	73.5	4.1	431	2	S37775	filamin, muscle -	1231	73	4.0	3011	1	S40770	genome polyprotein
1159	73.5	4.1	505	2	AC3486	cell surface prote	1232	73	4.0	3263	2	E82410	hypothetical prote
1160	73.5	4.1	579	2	B84956	cell division prot	1233	73	4.0	4688	2	F82885	hypothetical prote
1161	73.5	4.1	632	2	C98264	5'-nucleotidase pr	1234	73	4.0	4936	2	AH2515	hypothetical prote
1162	73.5	4.1	636	2	AF3020	5'-nucleotidase li	1235	72.5	4.0	124	2	S40364	Ig kappa chain - h
1163	73.5	4.1	677	2	T40145	probable beta-adap	1236	72.5	4.0	126	2	S40312	Ig kappa chain - h
1164	73.5	4.1	725	2	C87485	COMEC/Rec2 family	1237	72.5	4.0	128	2	S20636	Ig kappa chain V r
1165	73.5	4.1	815	2	E70021	3-hydroxyacyl-CoA	1238	72.5	4.0	137	2	E34903	Ig heavy chain pre
1166	73.5	4.1	941	2	S29043	cellulase (EC 3.2.	1239	72.5	4.0	141	2	T47178	Ig heavy chain var
1167	73.5	4.1	986	2	B1675	polymorphic membra	1240	72.5	4.0	198	2	T19797	hypothetical prote
1168	73.5	4.1	1005	2	T18537	Ig heavy chain - c	1241	72.5	4.0	199	2	G75153	hypothetical prote
1169	73.5	4.1	1052	2	H83909	cell wall-associat	1242	72.5	4.0	215	2	I64004	hypothetical prote
1170	73.5	4.1	1119	2	A86340	protein F2D10.24 (1243	72.5	4.0	219	2	S38865	Ig kappa chain - m
1171	73.5	4.1	1121	2	I38127	phosphoprotein pho	1244	72.5	4.0	233	1	JU0284	Fc gamma (IgG) rec
1172	73.5	4.1	1280	2	T00365	hypothetical prote	1245	72.5	4.0	247	2	PQ0655	outer capsid spike
1173	73.5	4.1	1285	2	B72420	hypothetical prote	1246	72.5	4.0	247	2	PQ0656	outer capsid spike
1174	73.5	4.1	1292	2	G20229	galactose binding	1247	72.5	4.0	247	2	PQ0657	outer capsid spike
1175	73.5	4.1	1330	1	G0FFE	epidermal growth f	1248	72.5	4.0	264	2	P27579	T-cell receptor al
1176	73.5	4.1	1487	2	S15904	alpha-1 proteinase	1249	72.5	4.0	267	2	FL0064	T-cell receptor be
1177	73.5	4.1	1571	2	T00062	hypothetical prote	1250	72.5	4.0	286	2	S32480	hypothetical prote
1178	73.5	4.1	3328	2	T30835	breast cancer tumo	1251	72.5	4.0	288	2	S29690	Ig heavy chain VDJ
1179	73	4.0	126	2	S24704	Ig heavy chain V6	1252	72.5	4.0	289	2	G00031	B7 protein - red-c
1180	73	4.0	127	2	PH1224	Ig kappa chain pre	1253	72.5	4.0	312	2	D82690	adenine-specific m
1181	73	4.0	128	2	PH0445	Ig kappa chain pre	1254	72.5	4.0	322	2	T50167	hypothetical prote
1182	73	4.0	131	2	E25733	T-cell receptor al	1255	72.5	4.0	350	2	T21106	hypothetical prote
1183	73	4.0	132	2	A27632	T-cell receptor al	1256	72.5	4.0	377	2	T05453	trehalose-6-phosph
1184	73	4.0	133	1	K4HUJI	Ig kappa chain pre	1257	72.5	4.0	401	2	E87531	probable ABC trans
1185	73	4.0	145	2	T21651	T-cell receptor be	1258	72.5	4.0	408	2	D95417	hypothetical prote
1186	73	4.0	225	2	E82473	hypothetical prote	1259	72.5	4.0	423	2	E64436	hypothetical prote
1187	73	4.0	332	2	S25747	Ig lambda chain -	1260	72.5	4.0	428	2	B84964	adenosylmethionine
1188	73	4.0	332	2	G83458	sulfate-binding pr	1261	72.5	4.0	451	2	T48340	hypothetical prote
1189	73	4.0	349	2	T08782	serine-type D-Ala-	1262	72.5	4.0	453	2	C31933	Ig mu chain C regi
1190	73	4.0	389	2	B42708	hypothetical prote	1263	72.5	4.0	475	2	S01321	Ig gamma-2b chain
1191	73	4.0	393	1	HVRKCI	Ig mu chain C regi	1264	72.5	4.0	482	2	T49079	serine-type carbox
1192	73	4.0	438	1	HVRKC2	Ig mu chain C regi	1265	72.5	4.0	498	2	G72729	protein containing
1193	73	4.0	445	2	S67695	26S proteasome reg	1266	72.5	4.0	503	2	B72289	oligopeptide ABC t
1194	73	4.0	451	1	S75239	hypothetical prote	1267	72.5	4.0	527	2	T22000	hypothetical prote
1195	73	4.0	454	2	A51970	hypothetical prote	1268	72.5	4.0	533	2	A42249	aspartic proteinas
1196	73	4.0	469	1	P2WL35	L2 protein - human	1269	72.5	4.0	560	2	B81451	flagellar M-ring p
1197	73	4.0	469	2	S36525	L2 protein - human	1270	72.5	4.0	668	2	T05803	hypothetical prote

1271	72.5	4.0	676	2	F69276	conserved hypother	1344	72	4.0	992	2	T46137	hypothetical prote
1272	72.5	4.0	735	2	D96830	probable heat-shoc	1345	72	4.0	1076	1	A35622	nuclear pore prote
1273	72.5	4.0	759	1	B60008	RNA-directed RNA p	1346	72	4.0	1083	2	S48460	probable membrane
1274	72.5	4.0	836	2	A69550	hypothetical prote	1347	72	4.0	1106	2	A97647	cation efflux syst
1275	72.5	4.0	887	1	IJCHCL	E-cadherin precurs	1348	72	4.0	1106	2	AG2870	AcR family transpo
1276	72.5	4.0	894	2	S61015	hypothetical prote	1349	72	4.0	1132	2	H90834	host specificity p
1277	72.5	4.0	941	2	F97353	uncharacterized co	1350	72	4.0	1149	2	T27567	hypothetical prote
1278	72.5	4.0	954	2	S57108	hypothetical prote	1351	72	4.0	1155	2	H71456	probable pyrolysin
1279	72.5	4.0	970	2	I78842	receptor protein-t	1352	72	4.0	1199	2	S77082	pyruvate (flavodox
1280	72.5	4.0	1039	2	T15885	hypothetical prote	1353	72	4.0	1245	1	VHWVB2	structural polypro
1281	72.5	4.0	1166	2	T29009	hypothetical prote	1354	72	4.0	1391	2	S50608	hypothetical prote
1282	72.5	4.0	1186	2	T42729	histocompatibility	1355	72	4.0	1408	2	H69068	cell surface glyco
1283	72.5	4.0	1212	2	T42387	histocompatibility	1356	72	4.0	2094	2	S33124	tpr protein - huma
1284	72.5	4.0	1228	2	G90581	hypothetical prote	1357	72	4.0	2567	2	A49551	filamin, Muller ce
1285	72.5	4.0	1229	2	T25697	hypothetical prote	1358	72	4.0	2902	2	C71953	toxin-like outer m
1286	72.5	4.0	1276	2	B86546	polymorphic oute	1359	72	4.0	3890	2	C89921	hypothetical prote
1287	72.5	4.0	1306	2	C81591	polymorphic membra	1360	72	4.0	8563	2	T30226	polyketide synthas
1288	72.5	4.0	1306	2	S22624	aggregation protei	1361	71.5	4.0	91	2	S17628	Ig kappa chain v r
1289	72.5	4.0	1383	2	T13052	guanine nucleotide	1362	71.5	4.0	119	2	PH1503	Ig heavy chain v r
1290	72.5	4.0	1431	2	A45866	dextranucrase (EC	1363	71.5	4.0	121	2	S44113	Ig kappa chain - h
1291	72.5	4.0	1500	1	QJ1348	carbamoyl-phosphat	1364	71.5	4.0	129	2	S40347	Ig kappa chain pre
1292	72.5	4.0	1665	2	T29008	hypothetical prote	1365	71.5	4.0	225	2	AL0029	myelin P0 protein
1293	72.5	4.0	1962	2	T08991	hypothetical prote	1366	71.5	4.0	246	1	A32999	PP31 protein - fow
1294	72.5	4.0	2004	2	F95133	immunoglobulin A1	1367	71.5	4.0	275	2	H35216	hypothetical prote
1295	72.5	4.0	2052	2	C97038	phage-related prot	1368	71.5	4.0	290	2	T40852	cystathionine beta
1296	72.5	4.0	3924	2	S37431	ankyrin 2, neutro	1369	71.5	4.0	303	2	H71693	hypothetical prote
1297	72.5	4.0	4845	2	T13067	BIR repeat contain	1370	71.5	4.0	305	2	B84413	hypothetical prote
1298	72	4.0	115	1	KVMSR2	Ig kappa chain pre	1371	71.5	4.0	321	2	F71163	probable oligopept
1299	72	4.0	115	2	A30995	T-cell receptor be	1372	71.5	4.0	325	2	H90269	hypothetical prote
1300	72	4.0	131	2	B34904	Ig kappa chain pre	1373	71.5	4.0	326	1	G2HU	Ig gamma-2 chain C
1301	72	4.0	131	2	B30577	Ig kappa chain pre	1374	71.5	4.0	340	2	S20879	homeotic protein H
1302	72	4.0	133	2	I45927	membrane-bound imm	1375	71.5	4.0	360	2	H95980	probable uroporph
1303	72	4.0	148	2	PH0121	Ig heavy chain pre	1376	71.5	4.0	361	2	S78542	drbpglucose 4,6-de
1304	72	4.0	148	2	WNV15	Ig heavy chain pre	1377	71.5	4.0	384	2	A12962	cellulose syntheti
1305	72	4.0	208	1	PHN15	18.5K protein - Au	1378	71.5	4.0	389	2	E98320	hypothetical prote
1306	72	4.0	223	2	I46696	CTLA-4 precursor -	1379	71.5	4.0	476	2	A46118	myosin-binding pro
1307	72	4.0	239	2	F81795	probable periplasm	1380	71.5	4.0	477	2	JC4386	adenylyl cyclase-a
1308	72	4.0	338	2	A53086	CCAAT enhancer-bin	1381	71.5	4.0	493	2	S39299	hexon protein - hu
1309	72	4.0	340	2	T02639	G5 protein homolog	1382	71.5	4.0	507	1	A43387	polymerase-associ
1310	72	4.0	349	2	F70357	lipoprotein - Aqu	1383	71.5	4.0	507	2	AC3036	glycerol-3-phospha
1311	72	4.0	351	2	QJ2166	spindle body prote	1384	71.5	4.0	507	2	H98249	glpD gene homolog
1312	72	4.0	372	1	UHUCUN	ciliary neurotroph	1385	71.5	4.0	520	2	A13295	adenylosuccinate s
1313	72	4.0	375	2	A64398	hypothetical prote	1386	71.5	4.0	523	1	S48997	IMP dehydrogenase
1314	72	4.0	386	2	B84582	probable tub famil	1387	71.5	4.0	523	1	S48997	Ig Y heavy chain (
1315	72	4.0	411	1	VBEGE2	Glycoprotein G pre	1388	71.5	4.0	572	2	B46529	purH bifunctional
1316	72	4.0	411	2	A37755	xylanase (EC 3.2.1	1389	71.5	4.0	592	2	JC4642	hypothetical prote
1317	72	4.0	424	2	H96963	dihydroorotase [im	1390	71.5	4.0	608	2	T32708	glutamine-fructose
1318	72	4.0	425	2	AC2959	HLyD family secret	1391	71.5	4.0	611	2	T45493	glutamine-binding
1319	72	4.0	428	2	T08626	sarcosine reductas	1392	71.5	4.0	647	2	F70057	penicillin-binding
1320	72	4.0	430	2	T32055	hypothetical prote	1393	71.5	4.0	659	2	S36551	El protein - human
1321	72	4.0	433	2	S76485	hypothetical prote	1394	71.5	4.0	668	2	T44118	penicillin-binding
1322	72	4.0	441	2	AF0048	modification methy	1395	71.5	4.0	668	2	JQ0774	phosphoribosylform
1323	72	4.0	452	2	C98334	hypothetical prote	1396	71.5	4.0	751	2	A13392	glutamine-tRNA lig
1324	72	4.0	454	2	A46532	Ig mu chain C regi	1397	71.5	4.0	775	1	I37422	transposable eleme
1325	72	4.0	513	2	D96943	probable polygalac	1398	71.5	4.0	775	2	A32494	hypothetical prote
1326	72	4.0	513	2	AH2996	glycerol-3-phospha	1399	71.5	4.0	776	2	S59790	leucyl-CRNA synth
1327	72	4.0	531	2	A98287	glpD gene homolog	1400	71.5	4.0	860	2	AC0582	protein F1504.39 l
1328	72	4.0	531	2	T50964	related to RCC1 pr	1401	71.5	4.0	893	2	F86476	hypothetical prote
1329	72	4.0	570	2	A57535	intrileukin 1 recep	1402	71.5	4.0	928	2	C97728	Na+/Ca2+-exchangin
1330	72	4.0	570	2	T46261	hypothetical prote	1403	71.5	4.0	958	2	S32435	hypothetical prote
1331	72	4.0	574	2	B64414	hypothetical prote	1404	71.5	4.0	1021	2	T15765	RNA-directed DNA p
1332	72	4.0	576	2	G81657	DNA mismatch repai	1405	71.5	4.0	1025	2	T10259	protein T06A10.1 l
1333	72	4.0	627	2	S14683	Ig mu chain precur	1406	71.5	4.0	1031	2	D88912	hypothetical prote
1334	72	4.0	665	2	F97032	beta-glucosidase f	1407	71.5	4.0	1031	2	T33655	DNA-directed DNA p
1335	72	4.0	697	2	T27587	hypothetical prote	1408	71.5	4.0	1094	2	S22573	TonB-dependent rec
1336	72	4.0	777	1	TVPPCP	large T antigen -	1409	71.5	4.0	1125	2	H87644	plasmid replicatio
1337	72	4.0	782	2	S22560	large T antigen -	1410	71.5	4.0	1128	1	T08322	insulin receptor s
1338	72	4.0	844	2	T37690	hypothetical prote	1411	71.5	4.0	1231	2	S30185	probable nuclear e
1339	72	4.0	844	2	T52396	formin-binding pro	1412	71.5	4.0	1250	2	T40062	CRAG protein - fru
1340	72	4.0	868	2	D86349	hypothetical prote	1413	71.5	4.0	1441	2	T13717	polyketide synthas
1341	72	4.0	878	1	REXS1B	RNA-directed RNA p	1414	71.5	4.0	1446	2	S73013	Subtilase family p
1342	72	4.0	892	2	T06818	DNA topoisomerase	1415	71.5	4.0	1448	2	AI2007	WD-40 repeat prote
1343	72	4.0	984	2	C84781	hypothetical prote	1416	71.5	4.0	1526	2	AC2239	

[illegible]

neural cell adhesion molecule long domain form precursor - chicken

N:Alternate names: NCAM-180
N:Contents: neural cell adhesion molecule, short domain form (NCAM-180)
C:Species: Gallus gallus (chicken)
C:Date: 31-Mar-1993 #sequence revision 31-Mar-1993 #text change 09-Mar-1993
C:Accession: A33613; A33613; A25435; B25435; A46550; S36350; A44366
F:Cunningham, B.A.; Hemperly, J.J.; Murray, B.A.; Prediger, E.A.; Science 236, 799-806, 1987
A:Title: Neural cell adhesion molecule: structure, immunoglobulin-like domain
A:Reference number: A33613; MUID:87206190; PMID:3576199
A:Accession: A33613
A:Molecule type: mRNA
A:Residues: 1-175 <CU2>
A:Cross-references: UNIPROT:P13590; UNIPARC:UPI0000174387; GB:M158
A:Accession: B43613
A:Molecule type: protein
A:Residues: 20-44120-127; 202-221; 320-342; 399-415; 640-659; 822-828
A:Cross-references: UNIPARC:UPI0000174388; UNIPARC:UPI00000174389;
A:Note: Asn-222 probably binds carbohydrate; Asn-426 probably does
F:Hempely, J.J.; Murray, B.A.; Edelman, G.M.; Cunningham, B.A.
Proc. Natl. Acad. Sci. U.S.A. 83, 3037-3041, 1986
A:Title: Sequence of a cDNA clone encoding the polysialic acid-rich
A:Reference number: A25435; MUID:86206089; PMID:3458261

A:Molecule type: mRNA
A:Residues: 128-1091 <HEM>
A:Cross-references: UNIPARC:UPI000017438F; GB:M13210
A:Accession: B25435
A:Molecule type: protein
A:Residues: 128-140:222-240:428-439:611-631:744-760:763-781:1080-1084 <HE2>
A:Cross-references: UNIPARC:UPI0000174390; UNIPARC:UPI0000174391; UNIPARC:UPI0000174392;
R;Murray, B.A.; Owens, G.C.; Prediger, E.A.; Crossin, K.L.; Cunningham, B.A.; Edelman, C.
J. Cell Biol. 103, 1431-1439, 1986
A:Title: Cell surface modulation of the neural cell adhesion molecule resulting from al
A:Reference number: A46550; MUID:87033934; PMID:3771645
A:Accession: A46550
A:Molecule type: DNA
A:Residues: 810-1070 <MUR>
A:Cross-references: UNIPARC:UPI0000174397; GB:X04479
R;Sagner, M.; Covault, J.
submitted to the EMBL Data Library, February 1993
A:Reference number: S36950
A:Accession: S36950
A:Molecule type: protein
A:Residues: 1-17 <SAS>
A:Cross-references: UNIPARC:UPI0000171377; EMBL:X70342; NID:9417631; PIDN:CAA49807.1; PI
R;Colwell, G.; Li, B.; Forrest, D.; Brackenbury, R.
Genomics 14, 875-882, 1992
A:Title: Conserved regulatory elements in the promoter region of the N-CAM gene.
A:Reference number: A44369; MUID:9312797; PMID:11478668
A:Accession: A44369
A:Molecule type: DNA
A:Residues: 1-17 <COF>
A:Cross-references: UNIPARC:UPI0000171377; EMBL:Z12128; NID:963653; PIDN:CAA78113.1; PID
R;Cole, G.J.; Loewy, A.; Cross, N.V.; Akeson, R.; Glaser, L.
J. Cell Biol. 103, 1739-1744, 1986
A:Title: Topographic localization of the heparin-binding domain of the neural cell adhe
A:Reference number: A60852; MUID:87057627; PMID:2430978
A:Accession: A60852
A:Molecule type: protein
A:Residues: 20-29 <COL>
A:Cross-references: UNIPARC:UPI0000174398
R;Rao, Y.; Wu, X.F.; Garlepy, J.; Rutishauser, U.; Siu, C.H.
J. Cell Biol. 118, 937-949, 1992
A:Title: Identification of a peptide sequence involved in homophilic binding in the neur
A:Reference number: A43280; MUID:92363934; PMID:1380002
A:Contents: annotation; homophilic binding region
C:Comment: NCAM mediates cell-cell adhesion via homophilic binding with another NCAM mol
C:Superfamily: Various forms of NCAM are produced by alternative splicing.
C:Keywords: neural cell adhesion molecule; fibronectin type III repeat homology; immu
P;1-19/Domain: alternative splicing; brain; cell adhesion; duplication; heparin binding; si
F;20-1091/Product: neural cell adhesion molecule, long domain form #status experimental
F;20-809,1071-1091/Product: neural cell adhesion molecule, short domain form #status exp
F;20-711/Domain: extracellular #status predicted <EXT>
F;34-98/Domain: immunoglobulin homology <IMM1>
F;132-191/Domain: immunoglobulin homology <IMM2>
F;152-156/Region: heparin binding #status predicted
F;161-165/Region: heparin binding #status predicted
F;228-289/Domain: immunoglobulin homology <IMM3>
F;262-271/Region: NCAM binding #status experimental
F;322-387/Domain: immunoglobulin homology <IMM4>
F;419-481/Domain: immunoglobulin homology <IMM5>
F;518-595/Domain: fibronectin type III repeat homology <FN3A>
F;624-685/Domain: fibronectin type III repeat homology <FN3B>
F;712-729/Domain: transmembrane #status predicted <IMM>
F;730-1091/Domain: intracellular #status predicted <INT>
F;41-96,139-189,329-385,426-479/Diulfide bonds: #status predicted
F;222/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;335,347,423,449,478/Binding site: carbohydrate (Asn) (covalent) #status predicted

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Db 256 QEDNEKYSFNDGSELIIKKVDKSDAEAYICIAENKAGEQDATIHLKVFAPKPIYVEN 315
QY 144 DISINEGNNISITCTATGPEPTVTW----RHISPKAV---GFVSEDEYLEIQGITREQ- 195
Db 316 KTAMELEDOITITCEASGDPISITWKTSRISNEEKTLDGRIVVRSHARVSSLLTKEI 375
QY 196 ----SGDYECASNDVAAPVRRVKVTNYPPIYSEAKGTGVPVGQKGTLOCEASAVPSA 251
Db 376 QYTDAGEYVCTASNTIGQD-SQAMYLEVQYAPKLOGPVAVYTWEGVQNVITCEVFAPSA 434
QY 252 EFQWKDKRLIEGK-KGVKVENRPLSKLIIFNTVSEHDYGNVTCVASKLGHNTNASIML 310
Db 435 VISWFRDQQLPSSNYSNIKIYTPSASYLEVTPDSEDFGNVYCTAVNRIQGESSEFIL 494
RESULT 13
T42633
connectin/titin - chicken (fragment)
C:Species: Gallus gallus (chicken)
C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
C;Accession: T42633
R;Tajima, H.; Ohtsuka, H.; Kawamura, Y.; Kume, H.; Murayama, T.; Abe, H.; Kimura, S.; Ma
Biochem. Biophys. Res. Commun. 223, 160-164, 1996
A:Title: A 11.5-kb 5'-terminal cDNA sequence of chicken breast muscle connectin/titin re
A:Reference number: Z22221; MUID:96254045; PMID:8660363
A:Accession: T42633
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-4162 <YAU>
A:Cross-references: UNIPROT:Q98918; UNIPARC:UPI000011025A; EMBL:D83390; NID:gl513029; PI
A:Experimental source: breast muscle
C:Keywords: skeletal muscle
Query Match 15.4%; Score 278.5; DB 2; Length 4162;
Best Local Similarity 27.3%; Pred. No. 8.7e-12;
Matches 78; Conservative 38; Mismatches 145; Indels 25; Gaps 7;
QY 37 TPBKMDNVTVRQGSATLRCTI-DNRVTRVAWLNRSITLYAGNDKWCLDPRVLLSNTQ 95
Db 3747 SFVKPEPENVLNGENITTSIVKSGPPLVKKWFRGSIELAPGHK-----CNIT 3795
QY 96 TOYSI---BIQNVDDVDEGYPYTCVQTDNHPKTSRVHLIVQVSPKIVEISSDISINEGNN 152
Db 3796 LQDSVAEELFDVQPLQSGDYTCQVSNKAGKISCTTHLFVKEPAKPFVPMKVDLSVEKGN 3855
QY 153 ISLTCATGPEPTVTW-----RHISPKAVGFVSEDEYLEIQGITREQSGDYECASN 205
Db 3856 LILECTYTGTPISVTWKNGVILKHSKCSITTTTSAILEIPNSKLEDDQGGYSCHIE 3915
QY 206 DVAAPVRRVKVTNYPPIY-ISEAKGTGVPVGQKGTLOCEASAVPSAEFQWKDKRLIE 264
Db 3916 DSGQDNCHGA-ITILEPPTFTVPLEPVQTVTGDASLQCVAGTPEMIVSWYKGDIKL-R 3973
QY 265 GKKGKVENRPLSKLIIFNVSEHDYGNVTCVASKLGHNTNASIML 310
Db 3974 GTATVKMHFKNQVATLVFQVSDSDSGEYICKVENTVGEATSSLL 4019
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IJRTNC
neural cell adhesion molecule short domain form precursor - rat
N;Alternate names: NCAM-140
C:Species: Rattus norvegicus (Norway rat)
C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004
C;Accession: S00846; B37795; I58136
R;Small, S.J.; Shull, G.E.; Santoni, M.J.; Akeson, R.
J. Cell Biol. 105, 2335-2345, 1987
A:Title: Identification of a cDNA clone that contains the complete coding sequence for a

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OM protein - protein search, using sw model

Run on: October 21, 2006, 17:58:51 ; Search time 302 Seconds
(without alignments)
1053.660 Million cell updates/sec

Title: US-09-981-915A-523
Perfect score: 1806
Sequence: 1 MKTIQPKMHNISWAIFTL.....RRAGCVMLPLVLHLLKF 344

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

Database : UniProt 7.2.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	1780	98.6	344	Q8BG33	MUS MUSCULUS
3	1665.5	92.2	344	1	NTRI_HUMAN
4	1647.5	91.2	344	1	NTRI_MOUSE
5	1641.5	90.9	344	2	Q3TYC2_MOUSE
6	1639.5	90.8	344	1	NTRI_RAT
7	1636	90.6	345	2	Q58DA5_BOVIN
8	1477.5	81.8	353	1	CEPUL_CHICK
9	1428	79.1	313	2	Q57592_CHICK
10	1427.5	79.0	344	2	Q91242_CHICK
11	1357.5	75.2	315	2	Q9DG15_CHICK
12	1306	72.3	337	2	Q6DFY2_MOUSE
13	1305	72.3	337	1	OBGAM_CHICK
14	1298	71.9	337	2	Q3TVL3_MOUSE
15	1295.5	71.7	338	2	Q723WC_HUMAN
16	1295.5	71.7	338	2	Q5R7T4_PONPY
17	1276.5	70.7	345	2	Q6GM08_XENLA
18	1275.5	70.6	344	2	Q9DF61_CHICK
19	1274	70.5	336	2	Q5ISA8_9PRIM
20	1270.5	70.3	344	2	Q6B0I4_HUMAN
21	1268	70.2	345	1	OPCM_HUMAN
22	1268	70.2	345	1	OPCM_PANTR
23	1266	70.1	345	1	OPCM_BOVIN
24	1259	69.7	345	1	OPCM_RAT
25	1251.5	69.3	319	2	Q5ISM6_MACFA
26	1137	63.0	231	2	Q3USC2_MOUSE
27	993.5	55.0	342	2	Q642G9_BRARE
28	946	52.4	334	2	Q02870_CHICK
29	938.5	52.0	338	1	LSAMP_CHICK
30	931.5	51.6	338	1	LSAMP_HUMAN
31	930.5	51.5	350	2	Q02869_GALLUS

Q62813	rattus norv	338	1	LSAMP_RAT
Q3TYE5	mus musculus	338	2	Q3TYE5_MOUSE
Q5M960	rattus norv	361	2	Q5M960_RAT
Q6GL27	xenopus lae	337	2	Q6GL27_XENLA
Q6BLK3	mus musculus	341	1	LSAMP_MOUSE
Q503N3	brachydanio	341	2	Q503N3_BRARE
Q2WF53	brachydanio	375	2	Q2WF53_BRARE
Q9W6V2	gallus galli	352	1	NEGR1_CHICK
Q5R412	pongo pygma	354	1	NEGR1_PONPY
Q723BI	homo sapien	354	1	NEGR1_HUMAN
Q2Z0J8	rattus norv	348	1	NEGR1_RAT
Q80Z24	mus musculus	348	1	NEGR1_MOUSE
Q4SL89	tetraodon n	325	2	Q4SL89_TETNG
Q8HW98	mus musculus	325	2	Q8HW98_MOUSE
Q4SUX1	tetraodon n	312	2	Q4SUX1_TETNG
Q8BMT5	mus musculus	188	2	Q8BMT5_MOUSE
Q4SDU6	tetraodon n	343	2	Q4SDU6_TETNG
Q8N440	homo sapien	226	2	Q8N440_HUMAN
Q568D3	brachydanio	227	2	Q568D3_BRARE
Q4SL88	tetraodon n	140	2	Q4SL88_TETNG
Q4S7M1	tetraodon n	193	2	Q4S7M1_TETNG
Q4V5E0	rosophila	536	2	Q4V5E0_DROME
Q9VMN6	rosophila	606	2	Q9VMN6_DROME
Q5TNT8	anopheles g	290	2	Q5TNT8_ANOGA
Q8IP70	rosophila	672	2	Q8IP70_DROME
Q9VLF0	rosophila	532	2	Q9VLF0_DROME
Q6NNU3	rosophila	532	2	Q6NNU3_DROME
Q9W4R3	rosophila	554	2	Q9W4R3_DROME
Q7Q864	anopheles g	301	2	Q7Q864_ANOGA
Q7Q0P9	anopheles g	340	2	Q7Q0P9_ANOGA
Q9VAR6	rosophila	413	2	Q9VAR6_DROME
Q4V3F0	rosophila	376	2	Q4V3F0_DROME
Q9VMB2	rosophila	315	2	Q9VMB2_DROME
Q5TQN9	anopheles g	317	2	Q5TQN9_ANOGA
Q7Q863	anopheles g	308	2	Q7Q863_ANOGA
Q9VMN9	rosophila	550	2	Q9VMN9_DROME
Q7Q0P8	anopheles g	351	2	Q7Q0P8_ANOGA
P91670	rosophila	528	2	P91670_DROME
Q7PRJ5	anopheles g	405	2	Q7PRJ5_ANOGA
Q9VCT4	rosophila	545	2	Q9VCT4_DROME
Q8WPB3	rosophila	316	2	Q8WPB3_DROSI
Q8WP94	rosophila	316	2	Q8WP94_DROSI
Q9VME2	rosophila	948	2	Q9VME2_DROME
Q7PN14	anopheles g	302	2	Q7PN14_ANOGA
Q8WP58	rosophila	315	2	Q8WP58_DROSI
P53664	rosophila	333	1	ANAL_DROME
Q7KX22	rosophila	341	2	Q7KX22_DROME
Q7PXA4	anopheles g	321	2	Q7PXA4_ANOGA
Q96RW7	homo sapien	5635	1	HMCN1_HUMAN
Q57577	cynops pyrr	846	2	Q57577_CYNPY
Q57576	cynops pyrr	1100	2	Q57576_CYNPY
Q9VP08	rosophila	400	2	Q9VP08_DROME
P13594	mus musculus	725	1	NCA11_MOUSE
P13595	mus musculus	1115	1	NCA11_MOUSE
Q921P2	mus musculus	605	2	Q921P2_MOUSE
Q8BQ96	mus musculus	839	2	Q8BQ96_MOUSE
Q8C4B2	mus musculus	839	2	Q8C4B2_MOUSE
Q3T1H3	rattus norv	849	2	Q3T1H3_RAT
Q5EA96	bos taurus	843	2	Q5EA96_BOVIN
Q512D5	canis fami	725	2	Q512D5_CANFA
Q73633	xenopus lae	725	2	Q73633_XENLA
Q512D7	canis fami	847	2	Q512D7_CANFA
NCAM1_CHICK	gallus galli	1091	1	NCAM1_CHICK
Q98918	gallus galli	4162	2	Q98918_CHICK
Q661V0	xenopus lae	719	2	Q661V0_XENLA
NCAM1_RAT	rattus norv	858	1	NCAM1_RAT
NCAM1_XENLA	rattus norv	1088	1	NCAM1_XENLA
Q6PFK4	brachydanio	405	2	Q6PFK4_BRARE
Q5ISL0	macaca fasc	690	2	Q5ISL0_MACFA
NCAL12_HUMAN	homo sapien	761	1	NCAL12_HUMAN
Q59FL7	homo sapien	276	15.3	Q59FL7_HUMAN
NCAL11_HUMAN	homo sapien	848	1	NCAL11_HUMAN
Q5R1Q0	felis silve	846	2	Q5R1Q0_FELCA

105	275.5	15.3	847	2	Q5G7G8_PELCA	Q5G7G8 felis silve	178	243.5	13.5	956	1	MAMC1_HUMAN	Q72553 homo sapien
106	275.5	15.3	853	1	NCAM1_BOVIN	P31836 bos taurus	179	243.5	13.5	1021	1	CNTN1_RAT	Q63198 rattus norv
107	274.5	15.1	857	2	Q512D6_CANFA	Q512D6 canis famil	180	243.5	13.5	1025	2	Q3UV20_MOUSE	Q3uv20 mus musculus
108	273.5	15.1	725	2	Q73634_XENLA	Q73634 xenopus lae	181	243.5	13.5	1036	1	CNTN2_CHICK	P28685 gallus gall
109	273	15.1	349	2	Q5T339_ANOGA	O5ts39 anopheles g	182	243.5	13.5	1278	2	Q4RRS5_TETNG	Q4rrs5 tetraodon n
110	272.5	15.1	433	2	Q6DJ83_XENTR	Q6dj83 xenopus tro	183	243	13.5	223	2	Q7QCH7_ANOGA	Q7qch7 anopheles g
111	272.5	15.1	1323	2	Q08476_CHICK	Q08476 gallus gall	184	242.5	13.4	949	1	MAMC1_RAT	P60756 rattus norv
112	271	15.0	858	2	Q86X47_HUMAN	Q86x47 homo sapien	185	241.5	13.4	837	1	NCAM2_HUMAN	O15394 homo sapien
113	270.5	15.0	1092	1	NCA12_XENLA	P36335 xenopus lae	186	241.5	13.4	1018	1	CNTN1_BOVIN	Q28106 bos taurus
114	270	15.0	1479	2	Q7KQT5_DROME	Q7kqt5 drosophila	187	241.5	13.4	1020	1	CNTN1_MOUSE	P12960 mus musculus
115	269.5	14.9	484	2	Q26475_SCHAM	Q26475 schistocerc	188	241	13.3	1100	2	Q5SRM8_MOUSE	Q5srkm8 mus musculus
116	268.5	14.9	722	2	Q4KMG2_HUMAN	Q4kmg2 homo sapien	189	240.5	13.3	948	2	Q7QCU0_ANOGA	Q7qcu0 anopheles g
117	268.5	14.9	1496	2	Q22626_HUMAN	Q22626 homo sapien	190	240	13.3	1693	2	Q4S6A5_TETNG	Q4s6a5 tetraodon n
118	268	14.8	1460	2	Q5H261_XENTR	Q5h261 xenopus tro	191	240	13.3	3707	1	PGBM_MOUSE	Q05793 mus musculus
119	268	14.8	5533	2	Q5RIP6_BRARE	Q5rip6 brachydanio	192	239	13.2	2528	2	Q4S2G3_TETNG	Q4s2g3 tetraodon n
120	265	14.7	1482	2	Q9V4Y0_DROME	Q9v4y0 drosophila	193	237.5	13.2	1054	1	LRIG2_MOUSE	Q51kr2 mus musculus
121	264.5	14.6	943	2	Q7PRK4_ANOGA	Q7prk4 anopheles g	194	237	13.1	312	2	Q66KV0_XENLA	Q66kv0 xenopus lae
122	263.5	14.6	323	2	Q7QBA7_ANOGA	Q7qba7 anopheles g	195	236.5	13.1	409	2	Q4SFV2_TETNG	Q4sfv2 tetraodon n
123	263	14.6	1431	2	Q80U60_MOUSE	Q80u60 mus musculus	196	235.5	13.0	632	2	Q6ZRK5_HUMAN	Q6zrk5 homo sapien
124	263	14.6	3950	2	Q7YRF5_CANFA	Q7yrf5 canis famil	197	235.5	13.0	1027	1	CNTN5_CHICK	Q90u79 gallus gall
125	262.5	14.5	829	2	Q4RIG0_TETNG	Q4rig0 tetraodon n	198	235.5	13.0	2623	2	Q6WR10_HUMAN	Q6wr10 homo sapien
126	261.5	14.5	437	2	Q81ZP8_HUMAN	Q81zp8 homo sapien	199	234.5	13.0	2752	2	Q7QKD0_ANOGA	Q7qkd0 anopheles g
127	261.5	14.5	1010	1	CNTN1_CHICK	P14781 gallus gall	200	234.5	13.0	358	2	Q90490_BRARE	Q90490 brachydanio
128	261	14.5	1031	2	Q90YM2_BRARE	Q90ym2 brachydanio	201	234.5	13.0	557	2	Q4RB52_TETNG	Q4rb52 tetraodon n
129	261	14.5	1395	2	Q44924_DROME	Q44924 drosophila	202	234.5	13.0	779	2	Q97136_MANSE	O97136 manduca sex
130	261	14.5	3410	2	Q7TN00_RAT	Q7tn00 rattus norv	203	234.5	13.0	837	2	Q97137_MANSE	O97137 manduca sex
131	260.5	14.4	400	2	Q7PZS8_ANOGA	Q7pzs8 anopheles g	204	234.5	13.0	1040	1	CNTN2_RAT	P22063 rattus norv
132	260.5	14.4	500	2	Q9W260_DROME	Q9w260 drosophila	205	234	13.0	1133	2	Q4T6R9_TETNG	Q4t6r9 tetraodon n
133	260.5	14.4	500	2	Q9XZB7_DROME	Q9xzb7 drosophila	206	233.5	12.9	1100	1	CNTN5_HUMAN	Q94779 homo sapien
134	260.5	14.4	862	2	Q4SST3_TETNG	Q4sst3 tetraodon n	207	233	12.9	394	1	IGS4B_XENLA	Q72xx1 xenopus lae
135	260	14.4	601	2	Q96CJ3_HUMAN	Q96cj3 homo sapien	208	233	12.9	1028	1	CNTN6_RAT	P97528 rattus norv
136	260	14.4	1395	2	Q7KVK3_DROME	Q7kvk3 drosophila	209	233	12.9	1049	2	Q4RM2_TETNG	Q4rm2 tetraodon n
137	260	14.4	1429	2	Q9W213_DROME	Q9w213 drosophila	210	233	12.9	1702	2	Q4RJ21_TETNG	Q4rj21 tetraodon n
138	259	14.3	7962	2	Q10465_HUMAN	Q10465 homo sapien	211	232.5	12.9	2693	2	Q8ISF3_CABEL	Q8isf3 caenorhabdi
139	259	14.3	34350	2	Q8W242_HUMAN	Q8w242 homo sapien	212	232.5	12.9	2708	2	Q8ISF4_CABEL	Q8isf4 caenorhabdi
140	258.5	14.3	395	2	Q8BXJ7_MOUSE	Q8bxj7 mus musculus	213	232.5	12.9	18519	2	Q8ISF6_CABEL	Q8isf6 caenorhabdi
141	258.5	14.3	395	2	Q8BZP4_MOUSE	Q8bzp4 mus musculus	214	232.5	12.9	18534	2	O8ISF7_CABEL	Q8isf7 caenorhabdi
142	258.5	14.3	404	2	Q8BLQ9_MOUSE	Q8blq9 mus musculus	215	231.5	12.8	858	2	O18466_HIRME	O18466 hirudo medi
143	258.5	14.3	404	2	Q8BYP1_MOUSE	Q8byp1 mus musculus	216	231.5	12.8	1005	2	P79921_XENLA	P79921 xenopus lae
144	257	14.2	1056	1	CNTN5_BRARE	Q72w34 brachydanio	217	231.5	12.8	1379	2	Q4SMF3_TETNG	Q4smf3 tetraodon n
145	256	14.2	435	2	Q8N3J6_HUMAN	Q8n3j6 homo sapien	218	231.5	12.8	5505	2	Q4RU89_TETNG	Q4ru89 tetraodon n
146	255.5	14.1	265	2	Q4V3R1_DROME	Q4v3r1 drosophila	219	231	12.8	703	2	Q21139_CABEL	Q21139 caenorhabdi
147	255.5	14.1	838	2	Q90YM1_BRARE	Q90ym1 brachydanio	220	231	12.8	1028	1	CNTN6_HUMAN	Q9uq52 homo sapien
148	255	14.1	359	1	LACH_DROME	Q24372 drosophila	221	231	12.8	1028	2	Q2KHM2_HUMAN	Q2khm2 homo sapien
149	255	14.1	1475	1	Q3UQ28_MOUSE	Q3uq28 mus musculus	222	230.5	12.8	459	2	Q3TAA6_MOUSE	Q3taa6 mus musculus
150	254.5	14.1	5175	2	Q81013_CABEL	Q81013 caenorhabdi	223	230.5	12.8	807	2	Q6NY23_BRARE	Q6ny23 brachydanio
151	254.5	14.1	5198	2	Q76518_CABEL	Q76518 caenorhabdi	224	230.5	12.8	868	1	MUSK_RAT	Q62838 rattus norv
152	253.5	14.0	404	2	Q3KQV9_HUMAN	Q3kqv9 homo sapien	225	230.5	12.8	868	2	Q3UOM3_MOUSE	Q3uom3 mus musculus
153	253.5	13.9	401	2	Q3VIM4_MOUSE	Q3vim4 mus musculus	226	230.5	12.8	887	2	Q3UGZ2_MOUSE	Q3ugz2 mus musculus
154	251.5	13.9	837	1	NCAM2_MOUSE	Q35136 mus musculus	227	230.5	12.8	932	2	Q3P9T5_MOUSE	Q3p9t5 mus musculus
155	250.5	13.9	377	2	Q5TNT9_ANOGA	Q5tn9 anopheles g	228	230.5	12.8	1032	2	Q8UVD6_BRARE	Q8uud6 brachydanio
156	250.5	13.9	1040	2	Q5RDT8_PONPY	Q5rdt8 pongo pygma	229	230.5	12.8	1040	1	CNTN2_MOUSE	Q61330 mus musculus
157	250.5	13.9	1342	2	Q9GPP6_DROME	Q9gpp6 drosophila	230	230.5	12.8	1040	2	Q3UH39_MOUSE	Q3uh39 mus musculus
158	250.5	13.9	1342	2	Q9VP27_DROME	Q9vp27 drosophila	231	230	12.7	1028	2	Q5R6D4_PONPY	Q5r6d4 pongo pygma
159	250	13.8	349	1	LACH_SCHAM	Q26474 schistocerc	232	229.5	12.7	510	2	Q801V8_BRARE	Q801v8 brachydanio
160	250	13.8	795	2	Q90YM0_BRARE	Q90ym0 brachydanio	233	229.5	12.7	773	2	Q32MJ8_HUMAN	Q32mj8 homo sapien
161	250	13.8	955	1	MDGAI_HUMAN	Q8nfp4 homo sapien	234	229.5	12.7	867	2	Q5VZW7_HUMAN	Q5vzw7 homo sapien
162	250	13.8	957	2	Q5TF58_HUMAN	Q5tf58 homo sapien	235	229.5	12.7	869	1	MUSK_HUMAN	O15146 homo sapien
163	249.5	13.8	1040	1	CNTN2_HUMAN	Q02246 homo sapien	236	229.5	12.7	875	2	Q5VZW8_HUMAN	Q5vzw8 homo sapien
164	249.5	13.8	1040	2	Q5T054_HUMAN	Q5t054 homo sapien	237	229	12.7	1056	2	Q90203_XENLA	Q90203 xenopus lae
165	247	13.6	204	2	Q7PUV5_ANOGA	Q7puj5 anopheles g	238	229	12.7	2331	2	Q59EG0_HUMAN	Q59eg0 homo sapien
166	246.5	13.6	627	2	Q5RDU0_PONPY	Q5rdn0 pongo pygma	239	229	12.7	4391	1	PGBM_HUMAN	Q98160 homo sapien
167	246.5	13.6	727	2	Q6RKB2_RAT	Q6rkb2 rattus norv	240	229	12.7	4391	2	Q5VU27_HUMAN	Q5vu27 homo sapien
168	246.5	13.6	837	2	Q6RKB3_RAT	Q6rkb3 rattus norv	241	228.5	12.7	866	2	Q2XY51_DROBR	Q2xy51 drosophila
169	246.5	13.6	865	2	Q68DA2_HUMAN	Q68da2 homo sapien	242	228.5	12.7	1040	2	Q9W675_BRARE	Q9w675 brachydanio
170	246.5	13.6	1018	1	CNTN1_HUMAN	Q12860 homo sapien	243	228.5	12.7	1117	1	LRIG3_MOUSE	O6pic6 mus musculus
171	245.5	13.6	292	2	Q4RFQ9_TETNG	Q4rfq9 tetraodon n	244	228	12.6	417	2	Q2TBL2_BOVIN	Q2tbl2 bos taurus
172	245.5	13.6	1033	2	Q4SB27_TETNG	Q4sb27 tetraodon n	245	228	12.6	900	2	Q4SR23_TETNG	Q4sr23 tetraodon n
173	245.5	13.6	1065	1	LRIG2_HUMAN	Q94898 homo sapien	246	228	12.6	1028	1	CNTN6_MOUSE	Q9jmb8 mus musculus
174	245	13.6	1028	2	Q6INB5_XENLA	Q6inb5 xenopus lae	247	228	12.6	1409	2	Q617L8_CABBR	Q617l8 caenorhabdi
175	244.5	13.5	3493	2	Q4RJ20_TETNG	Q4rj20 tetraodon n	248	227.5	12.6	1051	1	PTK7_CHICK	O91048 gallus gall
176	243.5	13.5	837	2	Q7Z7F2_HUMAN	Q7z7f2 homo sapien	249	227.5	12.6	1099	1	CNTN5_RAT	P97527 rattus norv
177	243.5	13.5	949	1	MAMC1_MOUSE	P60755 mus musculus	250	227	12.6	633	2	Q5W434_BRARE	Q5w434 brachydanio

251	227	12.6	651	2	Q5W433	brachydanio
252	227	12.6	1189	2	Q9P2J2	homo sapien
253	226.5	12.5	476	2	Q6AYP5	rattus norv
254	226.5	12.5	699	2	Q622N7_CABBR	caenorhabdi
255	226	12.5	8081	1	UNC89_CABEL	001761 caenorhabdi
256	225.5	12.5	860	2	Q32S49 MOUSE	Q32e49 mus musculus
257	225.5	12.5	868	1	MUSK MOUSE	Q61006 mus musculus
258	225.5	12.5	868	2	Q32S50 MOUSE	Q32e50 mus musculus
259	225.5	12.5	1070	2	Q4S2F2_TETNG	Q4s2f2 tetraodon n
260	225	12.5	881	2	Q4RQR3_TETNG	Q4rqr3 tetraodon n
261	224.5	12.4	783	2	Q32M3J9 HUMAN	Q32mj9 homo sapien
262	224.5	12.4	1208	2	Q2M3G2 HUMAN	Q2m3g2 homo sapien
263	224.5	12.4	1210	2	Q59FY0 HUMAN	Q59fy0 homo sapien
264	224.5	12.4	1224	2	Q00533 HUMAN	Q00533 homo sapien
265	224	12.4	1119	1	LRIG3 HUMAN	Q6uxm1 homo sapien
266	223.5	12.4	868	2	Q3TAX0 MOUSE	Q3tax0 mus musculus
267	223.5	12.4	868	2	Q3UP36 MOUSE	Q3up36 mus musculus
268	223	12.3	417	2	Q5R6B7 PONPY	Q5r6b7 pongo pygma
269	223	12.3	417	2	Q7TNL1 MOUSE	Q7tnl1 mus musculus
270	222.5	12.3	595	2	Q5W431 FUGRU	Q5w431 fugu rubrip
271	222.5	12.3	630	2	Q5W436 FUGRU	Q5w436 fugu rubrip
272	222.5	12.3	648	2	Q5W435 FUGRU	Q5w435 fugu rubrip
273	222.5	12.3	838	2	Q4SP99 TETNG	Q4sp99 tetraodon n
274	222.5	12.3	1639	2	Q3Y5G6 TRICA	Q3y5g6 tribolium c
275	222	12.3	450	2	Q9YR25 DROME	Q9yr25 drosophila
276	222	12.3	595	2	Q62RS5 HUMAN	Q62rs5 homo sapien
277	221.5	12.3	773	2	Q59FV3 HUMAN	Q59fv3 homo sapien
278	221.5	12.3	862	1	C022_MOUSE	P35329 mus musculus
279	221.5	12.3	867	2	Q2XY52 DROYA	Q2xy52 drosophila
280	221.5	12.3	867	2	Q2XY53 DROYA	Q2xy53 drosophila
281	221.5	12.3	867	2	Q2XY55 DROSI	Q2xy55 drosophila
282	221.5	12.3	870	2	Q2XY56 DROME	Q2xy56 drosophila
283	221	12.2	435	2	Q8WR44_CABEL	Q8wr44 caenorhabdi
284	221	12.2	436	2	Q8MPV1_CABEL	Q8mpv1 caenorhabdi
285	221	12.2	1340	2	Q8NDA2 HUMAN	Q8nda2 homo sapien
286	221	12.2	1746	2	Q8WY19 HUMAN	Q8wy19 homo sapien
287	221	12.2	1827	2	Q9VSG5 DROME	Q9vsg5 drosophila
288	221	12.2	2012	1	DSCAM HUMAN	O60469 homo sapien
289	221	12.2	2023	2	Q59GH3 HUMAN	Q59gh3 homo sapien
290	221	12.2	10495	2	Q4RE92 TETNG	Q4re92 tetraodon n
291	220.5	12.2	333	2	Q6QWB8 HUMAN	Q6qwb8 homo sapien
292	220.5	12.2	336	2	Q80VG4 MOUSE	Q80vg4 mus musculus
293	220.5	12.2	428	2	Q6F3J3 MOUSE	Q6f3j3 mus musculus
294	220.5	12.2	443	2	Q8N2F4 HUMAN	Q8n2f4 homo sapien
295	220.5	12.2	445	2	Q8K3T6 MOUSE	Q8k3t6 mus musculus
296	220.5	12.2	456	2	Q8R4L1 MOUSE	Q8r4l1 mus musculus
297	220.5	12.2	456	2	Q8R5M8 MOUSE	Q8r5m8 mus musculus
298	220.5	12.2	878	2	Q497X0 MOUSE	Q497x0 mus musculus
299	220.5	12.2	878	2	Q32SD3 MOUSE	Q32sd3 mus musculus
300	220.5	12.2	898	1	FAS2_SCHAM	P22648 schistocerc
301	220.5	12.2	1095	2	Q58EP4_BRARE	Q58ep4 brachydanio
302	220.5	12.2	1098	1	CNTN5_MOUSE	P68500 mus musculus
303	220	12.2	1043	2	Q6PA07_XENLA	Q6pa07 xenopus lae
304	220	12.2	1614	2	Q81VD7_XENLA	Q81vd7 xenopus lae
305	219.5	12.2	330	2	Q90Z42 CHICK	Q90z42 gallus gall
306	219.5	12.2	390	2	Q66KX2_XENLA	Q66kx2 xenopus lae
307	219.5	12.2	442	2	Q59Y67_HUMAN	Q59y67 homo sapien
308	219.5	12.2	617	2	Q49AF3 HUMAN	Q49af3 homo sapien
309	219.5	12.2	867	2	Q2XY54 DROSI	Q2xy54 drosophila
310	219.5	12.2	893	2	Q32SD4 MOUSE	Q32sd4 mus musculus
311	219.5	12.2	1012	2	Q4SW91_TETNG	Q4sw91 tetraodon n
312	219.5	12.2	1607	2	Q2M1J3_HUMAN	Q2m1j3 homo sapien
313	219	12.1	389	2	Q5U3R8_BRARE	Q5u3r8 brachydanio
314	219	12.1	1009	2	Q93250_XENLA	Q93250 xenopus lae
315	219	12.1	1026	1	CNTN4_HUMAN	Q81wv2 homo sapien
316	219	12.1	1062	2	Q8BK93_MOUSE	Q8bk93 m 15 days e
317	219	12.1	1091	1	LRIG1_MOUSE	P70193 mus musculus
318	219	12.1	1093	1	LRIG1_HUMAN	Q59ja1 homo sapien
319	219	12.1	1093	2	Q5XWD3_HUMAN	Q5xwd3 homo sapien
320	219	12.1	2222	2	Q4RY92 TETNG	Q4ry92 tetraodon n
321	219	12.1	4071	2	Q6KXZ1 CHICK	Q6kxz1 gallus gall
322	218.5	12.1	392	2	Q3UQW4_MOUSE	Q3uqw4 mus musculus
323	218.5	12.1	481	2	Q60ND3_CABBR	Q60nd3 caenorhabdi

324	218.5	12.1	1114	2	Q9BWV1_HUMAN	Q9bwv1 homo sapien
325	218.5	12.1	1115	2	Q6UXJ5_HUMAN	Q6uxj5 homo sapien
326	218.5	12.1	1612	1	ROBO1_MOUSE	Q89026 mus musculus
327	218	12.1	1753	2	Q2M0G8_DROPS	Q2m0g8 drosophila
328	218	12.1	2013	2	Q8VHZ8_RAT	Q8vzh8 rattus norv
329	218	12.1	2013	2	Q9ERC8_MOUSE	Q9erc8 mus musculus
330	217.5	12.0	348	2	Q00557_HUMAN	Q00557 homo sapien
331	217.5	12.0	626	2	Q4SMS6_TETNG	Q4sm56 tetraodon n
332	217.5	12.0	1759	2	Q7PPH8_ANOGA	Q7pph8 anopheles g
333	217	12.0	885	2	Q8HYV1_PIG	Q8hyv1 sus scrofa
334	217	12.0	886	2	Q8HYV2_PIG	Q8hyv2 sus scrofa
335	217	12.0	1443	2	Q8MTB2_DROME	Q8mtb2 drosophila
336	217	12.0	1765	2	Q9VS30_DROME	Q9vs30 drosophila
337	217	12.0	1770	2	Q9VS29_DROME	Q9vs29 drosophila
338	216.5	12.0	1048	2	Q7QH01_ANOGA	Q7qh01 anopheles g
339	216.5	12.0	1109	2	Q6P5H3_MOUSE	Q6p5h3 mus musculus
340	216.5	12.0	1937	2	Q7QGT8_ANOGA	Q7qgt8 anopheles g
341	216	12.0	435	2	Q5FWM6_XENLA	Q5fwm6 xenopus lae
342	215.5	11.9	886	2	Q9VM64_DROME	Q9vm64 drosophila
343	215.5	11.9	1302	1	NRG_DROME	P20241 drosophila
344	215.5	11.9	2597	2	Q6WRH9_RAT	Q6wrh9 rattus norv
345	215	11.9	410	2	Q3TQK2_MOUSE	Q3tqk2 mus musculus
346	215	11.9	443	2	Q8WR43_CABEL	Q8wr43 caenorhabdi
347	215	11.9	444	2	Q8MPU9_CABEL	Q8mpu9 caenorhabdi
348	215	11.9	904	2	Q7PME2_ANOGA	Q7pme2 anopheles g
349	215	11.9	1419	2	Q98SW3_BRARE	Q98sw3 brachydanio
350	214.5	11.9	816	2	Q8NFA5_HUMAN	Q8nfa5 homo sapien
351	214.5	11.9	1070	2	Q5T650_HUMAN	Q5t650 homo sapien
352	214.5	11.9	1070	2	Q6IQ54_HUMAN	Q6iq54 homo sapien
353	214.5	11.9	1651	1	ROBO1_RAT	Q55005 rattus norv
354	214	11.8	545	2	Q7QIV4_ANOGA	Q7qiv4 anopheles g
355	214	11.8	920	2	Q4RSG7_TETNG	Q4rsg7 tetraodon n
356	214	11.8	1026	1	CNTN4_MOUSE	Q69226 mus musculus
357	213.5	11.8	398	1	IGS4B_HUMAN	Q8n126 homo sapien
358	213.5	11.8	875	2	Q4RRR9_TETNG	Q4rrr9 tetraodon n
359	213.5	11.8	1028	1	CNTN3_HUMAN	Q9p232 homo sapien
360	213.5	11.8	1389	2	Q90Z69_BRARE	Q90z69 brachydanio
361	213	11.8	484	2	Q6BE00_XENLA	Q6be00 xenopus lae
362	213	11.8	1134	2	Q71B05_BRARE	Q71b05 brachydanio
363	212.5	11.8	1264	2	P91767_WANSE	P91767 manduca sex
364	212	11.7	1026	1	CNTN4_RAT	Q82845 rattus norv
365	212	11.7	1089	2	Q4S556_TETNG	Q4s556 tetraodon n
366	212	11.7	1151	2	Q9QVN5_SMURI	Q9qvn5 rattus sp.
367	211.5	11.7	773	2	Q6IDB4_DROME	Q6ide4 drosophila
368	211.5	11.7	873	1	FAS2_DROME	P34082 drosophila
369	211.5	11.7	1070	1	PTK7_HUMAN	Q13308 homo sapien
370	211.5	11.7	1102	2	Q923W7_MOUSE	Q923w7 mus musculus
371	211.5	11.7	1109	2	Q6AZB0_MOUSE	Q6azb0 mus musculus
372	211.5	11.7	1109	2	Q8CE91_MOUSE	Q8ce91 mus musculus
373	211.5	11.7	1110	2	Q8CE73_MOUSE	Q8ce73 mus musculus
374	211.5	11.7	1461	1	NEO1_HUMAN	Q82859 homo sapien
375	211	11.7	349	2	Q7QJG1_ANOGA	Q7qjg1 anopheles g
376	211	11.7	377	2	Q4RZV7_TETNG	Q4rzv7 mus musculus
377	211	11.7	396	1	IGS4B_MOUSE	Q99n28 mus musculus
378	211	11.7	1845	2	Q5MYA0_HUMAN	Q5mya0 homo sapien
379	211	11.7	6620	2	Q96AA2_HUMAN	Q96aa2 homo sapien
380	211	11.7	6620	2	Q5VST9_HUMAN	Q5vst9 homo sapien
381	210	11.6	588	2	Q4RFF0_TETNG	Q4rff0 tetraodon n
382	210	11.6	1561	2	Q924D2_MOUSE	Q924d2 mus musculus
383	210	11.6	1730	2	Q7YRQ7_PIG	Q7yrq7 sus scrofa
384	210	11.6	1914	1	MYLK_HUMAN	Q15746 homo sapien
385	210	11.6	1914	2	Q5MY99_HUMAN	Q5my99 homo sapien
386	210	11.6	1914	2	Q7Z4J0_HUMAN	Q7z4j0 homo sapien
387	210	11.6	1949	2	Q6PDN3_MOUSE	Q6pdn3 mus musculus
388	209.5	11.6	484	2	Q5QSL1_XENTR	Q5qsl1 xenopus tro
389	209	11.6	504	1	FGRL1_HUMAN	Q8n441 homo sapien
390	209	11.6	1030	2	Q8NFA8_HUMAN	Q8nfa8 homo sapien
391	209	11.6	2174	2	Q7QEG7_ANOGA	Q7qeg7 anopheles g
392	208.5	11.5	893	2	Q3TR55_MOUSE	Q3tres mus musculus
393	208.5	11.5	893	2	Q3UQ08_MOUSE	Q3uq08 mus musculus
394	208.5	11.5	1028	1	CNTN3_MOUSE	Q07409 mus musculus
395	208.5	11.5	1651	1	ROBO1_HUMAN	Q9y6n7 homo sapien
396	208	11.5	1280	2	Q4RRJ3_TETNG	Q4rrj3 tetraodon n

397	207.5	11.5	329	2	Q8N225_HUMAN	Q8n225 homo sapien	470	201	11.1	487	1	FGRL1_CHICK	Q7t2h2 gallus gall
398	207.5	11.5	1029	2	Q596X0_CARAU	Q596x0 carassius a	471	201	11.1	624	2	Q8BY18_MOUSE	Q8by18 mus musculu
399	207	11.5	452	2	Q5WRK1_CABEL	Q5wrk1 caenorhabdi	472	201	11.1	688	2	Q80ZE3_MOUSE	Q80ze3 mus musculu
400	207	11.5	600	2	Q8N7M7_HUMAN	Q8n7m7 homo sapien	473	201	11.1	700	1	KIRR2_MOUSE	Q7t2h2 mus musculu
401	207	11.5	1450	2	Q4SCT9_TETNG	Q4sct9 tetraodon n	474	201	11.1	946	2	Q07153_TORCA	Q07153 torpedo cal
402	207	11.5	2672	2	Q3UHH3_MOUSE	Q3uhh3 m 14 days p	475	201	11.1	1296	2	Q7QJ29_ANOGA	Q7qj29 anopheles g
403	206.5	11.4	915	2	Q8R4B3_MOUSE	Q8r4b3 mus musculu	476	201	11.1	1709	1	SN_HUMAN	Q9b2z2 homo sapien
404	206.5	11.4	952	2	Q4SPV1_TETNG	Q4spv1 tetraodon n	477	200.5	11.1	1708	2	Q7QH02_ANOGA	Q7qh02 anopheles g
405	206.5	11.4	1098	2	Q4RR11_TETNG	Q4rr11 tetraodon n	478	200.5	11.1	1271	2	Q6U714_BRARE	Q6u714 brachydanio
406	206.5	11.4	2016	2	Q9NBA1_DROME	Q9nba1 drosophila	479	200.5	11.1	1447	1	DCC_MOUSE	P70711 mus musculu
407	206	11.4	1055	2	Q61YV0_CABER	Q61yv0 caenorhabdi	480	200.5	11.1	1493	1	NEOI_MOUSE	P97798 mus musculu
408	206	11.4	1187	2	Q8WR45_CAEEL	Q8wr45 caenorhabdi	481	200.5	11.1	5516	2	Q7Z248_BRARE	Q7z248 brachydanio
409	205.5	11.4	1028	1	CNTN3_RAT	Q62682 rattus norv	482	200	11.1	524	2	Q7PSJ8_ANOGA	Q7psj8 anopheles g
410	205.5	11.4	2016	2	Q8MKM6_DROME	Q8mkm6 drosophila	483	200	11.1	1253	2	Q4SCT8_TETNG	Q4sct8 tetraodon n
411	205.5	11.4	2016	2	Q8MKM7_DROME	Q8mkm7 drosophila	484	199.5	11.0	1031	2	Q597F7_BRARE	Q597f7 brachydanio
412	205.5	11.4	2019	2	Q8MKM8_DROSOPHILA	Q8mkm8 drosophila	485	199.5	11.0	1209	2	Q7FG72_ANOGA	Q7fg72 anopheles g
413	205.5	11.4	17352	2	Q95YM2_PROCL	Q95ym2 procamburus	486	199.5	11.0	1215	2	Q7QEC1_ANOGA	Q7qec1 anopheles g
414	205	11.4	389	2	Q2VPF6_XENLA	Q2vpf6 xenopus lae	487	199.5	11.0	1445	2	Q63155_RAT	Q63155 rattus norv
415	204.5	11.3	439	2	Q57349_CHICK	Q57349 gallus gall	488	199.5	11.0	1465	2	Q7TQG5_MOUSE	Q7tqg5 mus musculu
416	204.5	11.3	1154	2	Q4SR22_TETNG	Q4sr22 tetraodon n	489	199	11.0	165	2	Q7Q8F3_ANOGA	Q7q8f3 anopheles g
417	204.5	11.3	1377	1	NEOI_RAT	P97603 rattus norv	490	199	11.0	440	2	Q6ZMD4_HUMAN	Q6zmd4 homo sapien
418	204.5	11.3	1675	2	Q9BSW4_BRARE	Q9bsw4 brachydanio	491	199	11.0	529	2	Q4SMH3_TETNG	Q4smh3 tetraodon n
419	204.5	11.3	3248	2	Q4SM90_TETNG	Q4sm90 tetraodon n	492	199	11.0	940	2	Q8NFA7_HUMAN	Q8nfa7 homo sapien
420	204.5	11.3	4129	2	Q59E65_DROME	Q59e65 drosophila	493	199	11.0	1241	1	NPHN_HUMAN	Q60500 homo sapien
421	204	11.3	335	2	Q5XKA0_XENLA	Q5xka0 xenopus lae	494	199	11.0	1513	2	Q9OZ70_BRARE	Q9oz70 brachydanio
422	204	11.3	437	2	Q7QGS8_ANOGA	Q7qgs8 anopheles g	495	199	11.0	1723	2	Q8CHB2_MOUSE	Q8chb2 mus musculu
423	204	11.3	478	2	Q4RVN0_TETNG	Q4rvn0 tetraodon n	496	198.5	11.0	931	2	Q6KAM5_MOUSE	Q6kam5 mus musculu
424	204	11.3	779	2	Q4STG7_TETNG	Q4stg7 tetraodon n	497	198	11.0	437	2	Q861V1_HUMAN	Q861v1 homo sapien
425	204	11.3	1000	2	Q4TBR4_TETNG	Q4tbr4 tetraodon n	498	198	11.0	662	2	Q6Q926_HUMAN	Q6q926 homo sapien
426	204	11.3	1443	1	NEOI_CHICK	Q90610 gallus gall	499	198	11.0	675	2	Q32M46_HUMAN	Q32m46 homo sapien
427	203.5	11.3	978	2	Q5TVT0_BRARE	Q5tv0 brachydanio	500	198	11.0	847	1	C222_HUMAN	P20273 homo sapien
428	203.5	11.3	1195	2	Q5TU52_ANOGA	Q5tu52 anopheles g	501	198	11.0	907	2	Q9NEG0_DROME	Q9neg0 drosophila
429	203.5	11.3	1228	2	Q7UE16_ANOGA	Q7ue16 anopheles g	502	198	11.0	1240	1	NPASC_RAT	P97885 rattus norv
430	203.5	11.3	1249	2	Q9OZ04_XENLA	Q9oz04 xenopus lae	503	198	11.0	2007	2	Q4SM88_TETNG	Q4sm88 tetraodon n
431	203.5	11.3	1285	2	Q5TY11_BRARE	Q5ty11 brachydanio	504	198	11.0	2024	2	Q53CM6_BRARE	Q53cm6 brachydanio
432	203.5	11.3	2053	1	DSCLI_HUMAN	Q8td84 homo sapien	505	197.5	10.9	293	2	Q3UUE8_MOUSE	Q3uee8 mus musculu
433	203.5	11.3	2645	2	Q4SLN8_TETNG	Q4sln8 tetraodon n	506	197.5	10.9	1164	2	Q66MN5_DROVI	Q66mn5 drosophila
434	203	11.2	483	2	Q7SX76_BRARE	Q7sx76 brachydanio	507	197.5	10.9	1228	2	Q8MRA3_DROME	Q8mra3 drosophila
435	203	11.2	912	2	Q4S2G4_TETNG	Q4s2g4 tetraodon n	508	197.5	10.9	1235	2	Q86BD5_DROME	Q86bd5 drosophila
436	203	11.2	1006	2	Q6IDE9_DROSOPHILA	Q6ide9 drosophila	509	197.5	10.9	1235	2	Q9V787_DROME	Q9v787 drosophila
437	203	11.2	1415	2	Q94155_CAEEL	Q94155 caenorhabdi	510	197.5	10.9	1240	1	NPASC_MOUSE	Q81u03 mus musculu
438	203	11.2	1950	2	Q8OVN8_MOUSE	Q8ovn8 mus musculu	511	197.5	10.9	1251	2	Q6ZQ54_MOUSE	Q6zq54 mus musculu
439	202.5	11.2	496	2	Q7Z075_CAEEL	Q7z075 caenorhabdi	512	197.5	10.9	1447	1	DCC_HUMAN	P43146 homo sapien
440	202.5	11.2	941	2	Q4SMD8_TETNG	Q4smd8 tetraodon n	513	197.5	10.9	16215	2	Q9NFS3_DROME	Q9nfs3 drosophila
441	202.5	11.2	1066	2	Q8MSR5_DROME	Q8msr5 drosophila	514	197.5	10.9	18074	2	Q917U4_DROME	Q917u4 drosophila
442	202.5	11.2	1946	2	Q68J72_APIME	Q68j72 apis mellif	515	197	10.9	1268	2	Q619L9_CABER	Q619l9 caenorhabdi
443	202.5	11.2	2828	2	Q9NR99_HUMAN	Q9nr99 homo sapien	516	196.5	10.9	1140	2	Q3TZP5_MOUSE	Q3tzp5 mus musculu
444	202	11.2	947	1	MUSK_CHICK	Q8axv6 gallus gall	517	196.5	10.9	1180	2	Q5IS40_PANTR	Q5is40 pan troglod
445	202	11.2	1269	2	Q01632_CAEEL	Q01632 caenorhabdi	518	196.5	10.9	1301	2	Q4RSG5_TETNG	Q4rsg5 tetraodon n
446	202	11.2	1273	2	Q49Z88_CAEEL	Q49z88 caenorhabdi	519	196	10.9	306	2	Q5HTT7_XENTR	Q5htt7 xenopus tro
447	202	11.2	1409	2	Q80IM2_BRARE	Q80im2 brachydanio	520	196	10.9	1347	1	NPASC_HUMAN	Q94856 homo sapien
448	202	11.2	1409	2	Q8J127_BRARE	Q8j127 brachydanio	521	196	10.9	1906	1	MYLK_CHICK	P11799 gallus gall
449	202	11.2	1428	2	Q8AY67_BRARE	Q8ay67 brachydanio	522	195.5	10.8	477	2	Q5EAJ2_FUGRU	Q5eaj2 fugu rubrip
450	202	11.2	1730	2	Q2VF24_PIG	Q2vf24 sus scrofa	523	195.5	10.8	1270	2	Q9U3P2_CAEEL	Q9u3p2 caenorhabdi
451	202	11.2	2022	2	Q7KQ05_DROME	Q7kq05 drosophila	524	195	10.8	489	2	Q4RM24_TETNG	Q4rm24 tetraodon n
452	201.5	11.2	232	2	Q7KQ08_ANOGA	Q7kq08 anopheles g	525	195	10.8	1369	1	NPASC_CHICK	Q42414 gallus gall
453	201.5	11.2	388	2	Q8NF28_HUMAN	Q8nf28 homo sapien	526	195	10.8	1375	2	Q8ML47_DROME	Q8ml47 drosophila
454	201.5	11.2	537	2	Q7QEY8_ANOGA	Q7qey8 anopheles g	527	195	10.8	1375	2	Q94537_DROME	Q94537 drosophila
455	201.5	11.2	786	2	Q4SR20_TETNG	Q4sr20 tetraodon n	528	195	10.8	1386	1	ROBO3_HUMAN	Q96m80 homo sapien
456	201.5	11.2	979	2	Q4TBUI_TETNG	Q4tbul tetraodon n	529	195	10.8	1526	2	Q94538_DROME	Q94538 drosophila
457	201.5	11.2	1421	2	Q49BB0_BRARE	Q49bb0 brachydanio	530	195	10.8	1526	2	Q9V6D5_DROME	Q9v6d5 drosophila
458	201.5	11.2	2008	2	Q3VEJ5_DROME	Q3vej5 drosophila	531	194.5	10.8	1277	1	L1CAM_FUGRU	Q9v902 fugu rubrip
459	201.5	11.2	2046	2	Q7KSE9_DROME	Q7kse9 drosophila	532	194	10.7	949	2	Q9VWZ7_DROME	Q9vwz7 drosophila
460	201.5	11.2	3215	2	Q8IRV7_DROME	Q8irv7 drosophila	533	194	10.7	1193	2	Q2VWP9_RAT	Q2vwp9 rattus norv
461	201.5	11.2	3262	2	Q9EQJ5_MOUSE	Q9eqj5 mus musculu	534	194	10.7	2095	2	Q4S8U5_TETNG	Q4s8u5 tetraodon n
462	201.5	11.2	4117	2	Q8IRV9_DROME	Q8irv9 drosophila	535	193.5	10.7	1256	1	NRCAM_MOUSE	Q81u04 mus musculu
463	201.5	11.2	4179	2	Q3W4V4_DROME	Q3w4v4 drosophila	536	193	10.7	749	2	Q967D9_DROME	Q967d9 drosophila
464	201.5	11.2	4223	2	Q8MPN3_DROME	Q8mpn3 drosophila	537	193	10.7	775	2	Q6PF50_XENLA	Q6pf50 xenopus lae
465	201.5	11.2	4228	2	Q8IRV8_DROME	Q8irv8 drosophila	538	193	10.7	803	2	Q80ZF5_RAT	Q80zf5 rattus norv
466	201.5	11.2	4629	2	Q9W4Y3_DROME	Q9w4y3 drosophila	539	193	10.7	902	2	Q81Q17_DROME	Q81q17 drosophila
467	201.5	11.2	8647	2	Q7KQP5_DROME	Q7kqp5 drosophila	540	193	10.7	903	2	Q967D8_DROME	Q967d8 drosophila
468	201.5	11.2	8930	2	Q7KQP7_DROME	Q7kqp7 drosophila	541	193	10.7	903	2	Q9VQY1_DROME	Q9vqy1 drosophila
469	201.5	11.2	8943	2	Q9V4F7_DROME	Q9v4f7 drosophila	542	193	10.7	949	2	Q8IGN3_DROME	Q8ign3 drosophila

543	193	10.7	1166	2	Q9QVN4_9MURI	Q9qvn4 rattus sp.
544	193	10.7	1508	2	Q6NR34_DROME	Q6nr34 drosophila
545	193	10.7	1508	2	Q9VQY2_DROME	Q9vqy2 drosophila
546	193	10.7	1531	2	Q967D7_DROME	Q967d7 drosophila
547	193	10.7	2029	1	LAR_DROME	Lar drosophila
548	192.5	10.7	200	2	Q4RRS2_TETNG	Q4rrs2 tetraodon n
549	192.5	10.7	776	2	Q4RHT1_TETNG	Q4rht1 tetraodon n
550	192.5	10.7	1150	2	Q2VMP7_HUMAN	Q2vmp7 homo sapien
551	192.5	10.7	1150	2	Q8BS24_MOUSE	Q8bs24 mus musculus
552	192.5	10.7	1209	2	P70232_MOUSE	P70232 mus musculus
553	192.5	10.7	1259	2	Q6PGJ3_MOUSE	Q6pgj3 mus musculus
554	192.5	10.7	1260	1	L1CAM_MOUSE	L1cam musculus
555	192.5	10.7	1284	1	NRCAM_CHICK	Nrcam chick
556	192	10.6	211	2	Q7PVK5_ANOGA	Q7pvk5 anopheles g
557	192	10.6	399	2	Q8N772_HUMAN	Q8n772 homo sapien
558	192	10.6	529	1	FGRL1_MOUSE	FGrl1 mus musculus
559	192	10.6	602	2	Q86YJ9_HUMAN	Q86yj9 homo sapien
560	192	10.6	606	2	Q4TK0_TETNG	Q4tk0 tetraodon n
561	192	10.6	650	2	Q8NAB4_HUMAN	Q8na84 homo sapien
562	192	10.6	771	2	Q4RMQ7_HUMAN	Q4rmq7 homo sapien
563	192	10.6	1256	2	Q35158_RAT	Q35158 rattus norv
564	192	10.6	1304	1	NRCAM_HUMAN	Nrcam homo sapien
565	192	10.6	1378	1	ROBO2_HUMAN	Robo2 homo sapien
566	191.5	10.6	1060	2	Q9QI13_RAT	Q9qiz13 rattus norv
567	191	10.6	1239	2	Q61PF2_CAEBR	Q61pf2 caenorhabdi
568	191	10.6	2154	2	Q8WZ51_HUMAN	Q8wz51 homo sapien
569	190.5	10.5	388	2	Q8A464_MOUSE	Q8a464 mus musculus
570	190.5	10.5	1154	2	Q9QVN3_9MURI	Q9qvn3 rattus sp.
571	190.5	10.5	1191	2	Q2VMP8_MOUSE	Q2vmp8 mus musculus
572	190.5	10.5	1194	2	Q6PW35_RAT	Q6pw35 rattus norv
573	190.5	10.5	1197	2	Q6PW37_RAT	Q6pw37 rattus norv
574	190.5	10.5	1198	2	Q6PW38_RAT	Q6pw38 rattus norv
575	190.5	10.5	1206	2	Q6PW36_RAT	Q6pw36 rattus norv
576	190.5	10.5	1209	2	Q6PW33_RAT	Q6pw33 rattus norv
577	190.5	10.5	1214	1	NRCAM_RAT	Nrcam rattus norv
578	190.5	10.5	1250	2	Q32MD9_MOUSE	Q32md9 mus musculus
579	190.5	10.5	1299	2	Q6PW34_RAT	Q6pw34 rattus norv
580	190.5	10.5	1366	1	ROBO3_MOUSE	Robo3 mus musculus
581	190.5	10.5	1441	2	Q3S3D7_XENBO	Q3s3d7 xenopus bor
582	190.5	10.5	4001	2	Q9NZP7_DROME	Q9n2p7 drosophila
583	190.5	10.5	4796	2	Q9W055_DROME	Q9w055 drosophila
584	190.5	10.5	4796	2	Q9N188_DROME	Q9n188 drosophila
585	190	10.5	345	2	Q811H7_MOUSE	Q811h7 mus musculus
586	190	10.5	381	2	Q9Y4A4_HUMAN	Q9y4a4 homo sapien
587	190	10.5	551	2	Q8NHN7_HUMAN	Q8nhn7 homo sapien
588	190	10.5	613	2	Q7PX10_ANOGA	Q7px10 anopheles g
589	190	10.5	1077	2	Q5WN88_CAEBR	Q5wn88 caenorhabdi
590	190	10.5	1090	2	Q4TAD5_TETNG	Q4tad5 tetraodon n
591	190	10.5	1406	2	Q9GPP7_DROME	Q9gpp7 drosophila
592	190	10.5	1463	2	Q9VQ08_DROME	Q9vq08 drosophila
593	189.5	10.5	433	2	Q9V644_DROME	Q9v644 drosophila
594	189.5	10.5	602	2	Q9VFD9_DROME	Q9vfd9 drosophila
595	189.5	10.5	765	2	Q9BKQ1_APLCA	Q9bkq1 aplysia cal
596	189.5	10.5	765	2	Q9TWA4_APLCA	Q9twa4 aplysia cal
597	189.5	10.5	812	2	Q9BKQ0_APLCA	Q9bkq0 aplysia cal
598	189.5	10.5	812	2	Q9TWA5_APLCA	Q9twa5 aplysia cal
599	189.5	10.5	880	2	Q7KPQ8_DROME	Q7kpq8 drosophila
600	189.5	10.5	932	2	Q9BKP9_APLCA	Q9bkp9 aplysia cal
601	189.5	10.5	932	2	Q9TWA6_APLCA	Q9twa6 aplysia cal
602	189.5	10.5	1180	2	Q5IS85_9PRIM	Q5is85 saimiri bol
603	189.5	10.5	1280	2	Q90933_CHICK	Q90933 gallus gall
604	189	10.5	595	2	Q7Q3K8_ANOGA	Q7q3k8 anopheles g
605	189	10.5	1238	2	Q59QC3_XENLA	Q59qc3 xenopus lae
606	189	10.5	1288	2	Q624K5_CAEBR	Q624k5 caenorhabdi
607	189	10.5	1340	2	Q5U176_DROME	Q5u176 drosophila
608	188.5	10.4	418	2	Q501T5_BRARE	Q501t5 brachydanio
609	188.5	10.4	1032	1	CNT1A_BRARE	Q8axz4 brachydanio
610	188.5	10.4	1187	2	Q589G5_CHICK	Q589g5 gallus gall
611	188.5	10.4	1328	2	Q4RKW3_TETNG	Q4rk3 tetraodon n
612	188.5	10.4	1390	1	CONT_DROME	Q9vni14 drosophila
613	188.5	10.4	1390	1	Q5BI91_DROME	Q5bi91 drosophila
614	188.5	10.4	2343	2	Q5TX11_ANOGA	Q5tx11 anopheles g
615	188	10.4	325	2	Q4SX51_TETNG	Q4sx51 tetraodon n

Q4taj7	tetraodon n
Q7lqm3	rattus norv
Q4v8p8	rattus norv
Q8ow68	mus musculus
Q9gqb1	xenopus lae
Q2uzub	aedes aegypt
Q311r5	homo sapien
Q4f90	tetraodon n
Q9yq7	mus musculus
Q5cnt4	anopheles g
Q3s3d8	xenopus bor
Q88971	mus musculus
Q5695	rattus norv
Q31696	gallus gall
Q7ztn4	xenopus lae
Q8izu9	homo sapien
Q3mi7	homo sapien
Q4vbk2	brachydanio
Q7tpd3	mus musculus
Q9qqr0	drosophila
Q696w0	brachydanio
Q7ph68	anopheles g
Q7pqg9	anopheles g
Q90413	brachydanio
Q4sl82	tetraodon n
Q14631	homo sapien
Q7q916	anopheles g
Q7q0x2	anopheles g
Q4spg3	tetraodon n
Q3tnw7	anopheles g
Q6uwl6	homo sapien
Q4rvz3	tetraodon n
Q8p61	xenopus lae
Q6nr91	drosophila
Q7kqp6	drosophila
Q86sn1	h soluble f
Q15109	homo sapien
Q311s0	homo sapien
Q61v11	caenorhabdi
P6731	homo sapien
Q8n4d0	homo sapien
Q4shh6	tetraodon n
Q8mmj9	bombyx mori
Q8t101	bombyx mori
Q7pvm1	anopheles g
Q50l7	brachydanio
Q8r4b5	mus musculus
Q8br86	mus musculus
Q6x936	rattus norv
Q8nhn0	homo sapien
Q8wz52	homo sapien
Q91562	xenopus lae
Q9hcd3	homo sapien
Q8c6w0	mus musculus
Q6gm29	xenopus lae
Q3tzm7	mus musculus
Q33g30	homo sapien
Q695l1	homo sapien
Q21y8	drosophila
P07722	rattus norv
Q53hd1	homo sapien
Q96j84	homo sapien
Q5w0f8	homo sapien
Q24327	drosophila
Q9v643	drosophila
Q8axb3	brachydanio
Q9vfu7	drosophila
Q4kmg0	homo sapien
Q7z5n4	homo sapien
Q4t680	tetraodon n
Q3t1f6	mus musculus
Q5e9n1	bos taurus

689	183	10.1	941	2	Q5J1R9_BRARE	Q5j1r9 brachydanio	762	178	9.9	379	2	Q9CWW1_MOUSE	Q9cww1 mus musculus
690	183	10.1	1232	2	Q90284_CARAU	Q90284 carassius a	763	178	9.9	413	1	HEMO_MANSE	P31398 manduca sex
691	183	10.1	1328	2	Q21043_CAEL	Q21043 caenorhabdi	764	178	9.9	492	2	Q9ET54_MOUSE	Q9et54 mus musculus
692	183	10.1	4816	2	Q8T103_BOMMO	Q8t103 bombyx mori	765	178	9.9	563	2	Q5FWR8_XENTR	Q5fwr8 xenopus tro
693	182.5	10.1	260	2	Q9XXD7_CAEL	Q9xxd7 caenorhabdi	766	178	9.9	853	2	Q6DFX7_MOUSE	Q6dfx7 mus musculus
694	182.5	10.1	363	2	Q5JP26_HUMAN	Q5jp26 homo sapien	767	178	9.9	1073	2	Q9TX18_CAEL	Q9tx18 caenorhabdi
695	182.5	10.1	931	2	Q8NF26_HUMAN	Q8nf26 homo sapien	768	178	9.9	1081	2	Q69ZT7_MOUSE	Q69zt7 mus musculus
696	182.5	10.1	997	2	Q44087_CAEL	Q44087 caenorhabdi	769	178	9.9	1400	2	Q7PF94_ANOGA	Q7pf94 anopheles g
697	182.5	10.1	1083	2	Q76698_CAEL	Q76698 caenorhabdi	770	177.5	9.8	344	2	Q9VY33_DROME	Q9vy33 drosophila
698	182.5	10.1	1098	2	Q961D6_DROME	Q961d6 drosophila	771	177.5	9.8	457	2	Q960D1_DROME	Q960d1 drosophila
699	182.5	10.1	1332	2	Q9BN17_DROME	Q9bn17 drosophila	772	177.5	9.8	583	1	CD166_BOVIN	Q9bhl3 bos taurus
700	182.5	10.1	1332	2	Q9VOW7_DROME	Q9vow7 drosophila	773	177.5	9.8	731	2	Q7PUQ1_ANOGA	Q7puq1 anopheles g
701	182.5	10.1	1336	1	VGER1_RAT	P53767 rattus norv	774	177.5	9.8	796	2	Q91287_PLEWA	Q91287 pleurodeles
702	182.5	10.1	1944	2	Q69513_BRARE	Q69513 brachydanio	775	177.5	9.8	1249	2	Q7TMZ9_RAT	Q7tmz9 rattus norv
703	182	10.1	582	2	Q56754_HUMAN	Q56754 mus musculu	776	177.5	9.8	1527	2	Q9VZ24_DROME	Q9vz24 drosophila
704	182	10.1	582	2	Q3ZB62_MOUSE	Q3zb62 mus musculu	777	177	9.8	376	2	Q90Z71_BRARE	Q90z71 brachydanio
705	182	10.1	609	2	Q3ZB61_MOUSE	Q3zb61 mus musculu	778	177	9.8	404	2	Q9Y3E9_HUMAN	Q9y3e9 homo sapien
706	182	10.1	626	1	NAG_HUMAN	P20916 homo sapien	779	177	9.8	410	2	Q4FAT1_BOMMO	Q4fat1 bombyx mori
707	182	10.1	626	1	Q53E57_HUMAN	Q53e57 homo sapien	780	177	9.8	467	2	Q4R5P0_MACFA	Q4r5p0 macaca fasc
708	182	10.1	661	2	Q59GD9_HUMAN	Q59gd9 homo sapien	781	177	9.8	474	2	Q5FV48_FUGRU	Q5fv48 fugu rubrip
709	182	10.1	877	2	Q9GSH3_HALIRO	Q9gsh3 halocynthia	782	177	9.8	577	2	Q80Y42_MOUSE	Q80y42 mus musculu
710	182	10.1	2212	2	Q8NHN3_HUMAN	Q8nhn3 homo sapien	783	177	9.8	1001	2	Q5TR64_ANOGA	Q5tr64 anopheles g
711	182	10.1	2224	2	Q4SLN7_TETNG	Q4sln7 tetraodon n	784	177	9.8	2242	2	Q9P2P9_HUMAN	Q9p2p9 homo sapien
712	182	10.1	17903	2	Q7RTL4_DROME	Q7rtl4 drosophila	785	177	9.8	8625	2	Q86GD6_PROCL	Q86gd6 procambarus
713	181.5	10.0	661	2	Q5RJW1_MOUSE	Q5rjw1 mus musculu	786	176.5	9.8	510	2	Q7L3E0_HUMAN	Q7l3e0 homo sapien
714	181.5	10.0	813	1	PUNC_MOUSE	Q8bqc3 mus musculu	787	176.5	9.8	686	1	SIG11_HUMAN	Q96rl6 homo sapien
715	181.5	10.0	1197	1	LICAI_BRARE	Q90478 brachydanio	788	176.5	9.8	772	2	Q9Y2J6_HUMAN	Q9y2j6 homo sapien
716	181.5	10.0	1333	1	VGER1_MOUSE	P35969 mus musculu	789	176.5	9.8	1106	2	Q8WX93_HUMAN	Q8wx93 homo sapien
717	181	10.0	593	2	Q5W0F9_HUMAN	Q5w0f9 homo sapien	790	176.5	9.8	1355	2	Q2XPT7_CANFA	Q2xpt7 canis fami
718	181	10.0	676	2	Q4SIF9_TETNG	Q4sif9 tetraodon n	791	176.5	9.8	2169	1	SDK1_CHICK	Q8av58 gallus gall
719	181	10.0	885	2	Q8N237_HUMAN	Q8n237 homo sapien	792	176.5	9.8	3165	2	Q70767_ANOGA	Q70767 anopheles g
720	181	10.0	913	2	Q8T3B5_CAEL	Q8t3b5 caenorhabdi	793	176	9.7	410	2	Q6R3L9_BOMMA	Q6r3l9 bombyx mand
721	181	10.0	928	2	Q19128_CAEL	Q19128 caenorhabdi	794	176	9.7	416	2	Q7Q1Z7_ANOGA	Q7q1z7 anopheles g
722	181	10.0	955	2	Q8MQ86_CAEL	Q8mq86 caenorhabdi	795	176	9.7	577	2	Q9D2Z1_MOUSE	Q9d2z1 m adult mal
723	181	10.0	1244	2	Q69YJ3_HUMAN	Q69yj3 homo sapien	796	176	9.7	964	2	Q18382_CAEL	Q18382 caenorhabdi
724	181	10.0	1263	2	Q7Z3B7_HUMAN	Q7z3b7 homo sapien	797	176	9.7	1319	2	Q4T8B2_TETNG	Q4t8b2 tetraodon n
725	181	10.0	3198	2	Q9U8G8_MANSE	Q9u8g8 manduca sex	798	175.5	9.7	1196	2	Q63210_CAEL	Q63210 caenorhabdi
726	181	10.0	5604	2	Q4ZG20_HUMAN	Q4zg20 homo sapien	799	175.5	9.7	1227	2	Q9BIA2_CAEL	Q9bia2 caenorhabdi
727	181	10.0	5604	2	Q8W253_HUMAN	Q8w253 homo sapien	800	175.5	9.7	1505	2	Q7Q623_ANOGA	Q7q623 anopheles g
728	180.5	10.0	848	2	Q25198_HYDAT	Q25198 hydra atten	801	175	9.7	234	2	Q8IZQ9_HUMAN	Q8izq9 homo sapien
729	180.5	10.0	1242	1	NPHN_MOUSE	Q9qz57 mus musculu	802	175	9.7	949	2	Q4SL83_TETNG	Q4sl83 tetraodon n
730	180.5	10.0	1256	2	Q925S5_MOUSE	Q925s5 mus musculu	803	175	9.7	1391	2	Q8N3L4_HUMAN	Q8n3l4 homo sapien
731	180.5	10.0	1256	2	Q9JIX1_MOUSE	Q9jix1 mus musculu	804	174.5	9.7	179	2	Q3Q260_HUMAN	Q3q260 homo sapien
732	180.5	10.0	1256	2	Q9ET59_MOUSE	Q9et59 mus musculu	805	174.5	9.7	409	2	Q3V5D4_XENLA	Q3v5d4 xenopus lae
733	180.5	10.0	1269	2	Q6U715_BRARE	Q6u715 brachydanio	806	174.5	9.7	529	2	Q3MU10_PONPY	Q3mu10 pongo pygma
734	180.5	10.0	1534	2	Q4ARRJ4_TETNG	Q4arrj4 tetraodon n	807	174.5	9.7	534	2	Q3V5Y8_9PRIM	Q3v5y8 gorilla gor
735	180	10.0	413	2	Q27418_MANSE	Q27418 manduca sex	808	174.5	9.7	1140	2	Q4RRD1_TETNG	Q4rrd1 tetraodon n
736	180	10.0	483	2	Q32LG4_BOVIN	Q32lg4 bos taurus	809	174.5	9.7	1250	2	Q624J4_CAEBR	Q624j4 caenorhabdi
737	180	10.0	571	2	Q5W0G0_HUMAN	Q5w0g0 homo sapien	810	174.5	9.7	1792	2	Q4SK53_TETNG	Q4sk53 tetraodon n
738	180	10.0	606	2	Q7QHA0_ANOGA	Q7qha0 anopheles g	811	174	9.6	452	2	Q4R5Y9_MACFA	Q4r5y9 macaca fasc
739	180	10.0	626	2	Q5R4C0_PONPY	Q5r4c0 pongo pygma	812	174	9.6	534	2	Q866T2_PANTR	Q866t2 pan troglod
740	180	10.0	917	2	Q2KHL7_MOUSE	Q2khl7 mus musculu	813	174	9.6	534	2	Q2VF35_PANTR	Q2vf35 pan troglod
741	180	10.0	1335	2	Q610C7_CAEBR	Q610c7 caenorhabdi	814	174	9.6	622	2	Q3TAG1_MOUSE	Q3tag1 mus musculu
742	180	10.0	18412	2	Q7ZZ61_BRARE	Q7zz61 brachydanio	815	174	9.6	626	2	Q53HA1_HUMAN	Q53ha1 homo sapien
743	179.5	9.9	333	2	Q90Z41_CHICK	Q90z41 gallus gall	816	174	9.6	630	2	Q7QBL9_ANOGA	Q7qbl9 anopheles g
744	179.5	9.9	362	2	Q3JH01_RAT	Q3jh01 rattus norv	817	174	9.6	675	2	Q7T0V5_XENLA	Q7t0v5 xenopus lae
745	179.5	9.9	503	2	Q9W259_DROME	Q9w259 drosophila	818	174	9.6	736	2	Q8MYS2_DROME	Q8mys2 drosophila
746	179.5	9.9	735	2	Q4RZ59_TETNG	Q4rzs9 tetraodon n	819	174	9.6	774	2	Q9V930_DROME	Q9v930 pongo pygma
747	179.5	9.9	804	2	Q80021_BRARE	Q80021 brachydanio	820	174	9.6	1255	2	Q7YQL7_PONPY	Q7yql7 pan troglod
748	179.5	9.9	806	2	Q90Z00_BRARE	Q90z00 brachydanio	821	174	9.6	1255	2	Q7YQL8_PANTR	Q7yql8 pan troglod
749	179	9.9	300	1	JAM1_MOUSE	Q88792 mus musculu	822	174	9.6	1721	2	Q961U1_DROME	Q961u1 drosophila
750	179	9.9	300	2	Q8VC39_MOUSE	Q8vc39 mus musculu	823	174	9.6	1748	2	Q4S3Q6_TETNG	Q4s3q6 tetraodon n
751	179	9.9	567	2	Q3ZB60_MOUSE	Q3zb60 mus musculu	824	174	9.6	2389	2	Q6BEQ6_CAEL	Q6beq6 caenorhabdi
752	179	9.9	626	1	NAG_MOUSE	P20917 mus musculu	825	174	9.6	3375	1	UNC52_CAEL	Q6s61 caenorhabdi
753	179	9.9	782	2	Q4SI43_TETNG	Q4si43 tetraodon n	826	174	9.6	4650	2	Q15598_HUMAN	Q15598 homo sapien
754	179	9.9	814	1	PUNC_HUMAN	Q8ivul homo sapien	827	174	9.6	658	2	Q76281_DROME	Q76281 drosophila
755	179	9.9	917	1	ICAM5_MOUSE	Q60625 mus musculu	828	173.5	9.6	360	2	Q8MRE6_DROME	Q8mre6 drosophila
756	179	9.9	1019	2	Q8BJK6_MOUSE	Q8bjk6 m 9 days em	829	173.5	9.6	363	2	Q3L1R7_HUMAN	Q3l1r7 homo sapien
757	179	9.9	3317	2	Q7QJK9_ANOGA	Q7qjk9 anopheles g	830	173.5	9.6	420	2	Q3L1R8_HUMAN	Q3l1r8 homo sapien
758	178.5	9.9	603	2	Q4SLP0_TETNG	Q4slp0 tetraodon n	831	173.5	9.6	442	2	Q6KAT6_MOUSE	Q6kat6 mus musculu
759	178.5	9.9	1234	1	NPHN_RAT	Q9r044 rattus norv	832	173.5	9.6	463	2	Q7PN36_ANOGA	Q7pn36 anopheles g
760	178.5	9.9	1252	2	Q9JIX2_RAT	Q9jix2 rattus norv	833	173.5	9.6	525	2	Q5R9N6_PONPY	Q5r9n6 pongo pygma
761	178.5	9.9	2293	2	Q4T1M4_TETNG	Q4t1m4 tetraodon n	834	173.5	9.6	538	2	Q9NNQ7_HUMAN	Q9nnq7 homo sapien

835	173.5	9.6	766	2	Q7Q0S7	ANOGA	Q7Q0S7	anopheles g
836	173.5	9.6	1021	2	P79757	CHICK	P79757	gallus gall
837	173.5	9.6	2680	2	Q7PXZ1	ANOGA	Q7PXZ1	anopheles g
838	173.5	9.6	4463	2	Q8MLD8	DROME	Q8MLD8	drosophila
839	173.5	9.6	9270	2	Q8MLD9	DROME	Q8MLD9	drosophila
840	173	9.6	385	2	Q9UQF5	HUMAN	Q9UQF5	homo sapien
841	173	9.6	410	2	Q6R3M0	BOMMO	Q6R3M0	bombyx mori
842	173	9.6	410	2	Q7YZA7	BOMMO	Q7YZA7	bombyx mori
843	173	9.6	410	2	Q6R3M2	BOMMO	Q6R3M2	bombyx mori
844	173	9.6	1248	2	Q9XT41	CERAE	Q9XT41	cercopitheca
845	172.5	9.6	279	2	Q2XQV0	MOUSE	Q2XQV0	mus musculus
846	172.5	9.6	357	2	Q8R112	MOUSE	Q8R112	mus musculus
847	172.5	9.6	1880	2	Q18465	HIRME	Q18465	hirudo medi
848	172	9.5	287	2	Q13984	HUMAN	Q13984	homo sapien
849	172	9.5	319	1	QPA333	MOUSE	QPA333	mus musculus
850	172	9.5	1045	2	Q5VV36	HUMAN	Q5VV36	homo sapien
851	172	9.5	1045	2	Q8TC37	HUMAN	Q8TC37	homo sapien
852	172	9.5	1320	2	Q5VV35	HUMAN	Q5VV35	homo sapien
853	172	9.5	1320	2	Q8ETC9	HUMAN	Q8ETC9	homo sapien
854	172	9.5	1320	2	Q96KFF	HUMAN	Q96KFF	homo sapien
855	172	9.5	2403	2	Q8MLD5	DROME	Q8MLD5	drosophila
856	172	9.5	4736	2	Q7YT98	MYTGA	Q7YT98	mytilus gal
857	172	9.5	7210	2	Q9V7G8	DROME	Q9V7G8	drosophila
858	171.5	9.5	283	2	Q9VT76	DROME	Q9VT76	drosophila
859	171.5	9.5	307	2	Q94431	CIOIN	Q94431	ciona intes
860	171.5	9.5	534	2	Q3V5Y9	PANPA	Q3V5Y9	pan paniscu
861	171.5	9.5	1338	1	VGFR1	HUMAN	P17948	h vascular
862	171.5	9.5	2772	2	Q9VAV3	DROME	Q9VAV3	drosophila
863	171.5	9.5	2894	2	Q4UX26	DROME	Q4UX26	drosophila
864	171.5	9.5	26326	2	Q4UI26	HUMAN	Q4UI26	homo sapien
865	171	9.5	373	2	Q7KYP5	HUMAN	Q7KYP5	homo sapien
866	171	9.5	464	2	Q16170	HUMAN	Q16170	homo sapien
867	171	9.5	468	2	Q9CA7	HUMAN	Q9CA7	homo sapien
868	171	9.5	493	2	Q3RCG8	HUMAN	Q3RCG8	homo sapien
869	171	9.5	526	1	CEAM1	HUMAN	P13688	homo sapien
870	171	9.5	534	2	Q8GE54	HUMAN	Q8GE54	homo sapien
871	171	9.5	810	2	Q9PS96	XENLA	Q9PS96	anopheles lae
872	171	9.5	917	2	Q3UY19	MOUSE	Q3UY19	mus musculus
873	171	9.5	937	2	Q5WN68	CAEBR	Q5WN68	caenorhabdi
874	171	9.5	1255	2	Q7Z329	HUMAN	Q7Z329	homo sapien
877	171	9.5	1257	1	SDK DROME		P32004	homo sapien
878	170.5	9.4	370	2	Q8WZB3	HUMAN	Q8WZB3	homo sapien
879	170.5	9.4	501	2	Q6Q147	BOVIN	Q6Q147	bos taurus
880	170.5	9.4	521	1	CD166	RABIT	Q48651	oryctolagus
881	170.5	9.4	540	2	Q8N029	HUMAN	Q8N029	homo sapien
882	170.5	9.4	591	2	Q6NPM0	DROME	Q6NPM0	drosophila
883	170.5	9.4	1197	2	Q4RVM1	TETNG	Q4RVM1	tetraodon n
884	170	9.4	255	2	Q6QVE7	CAEBR	Q6QVE7	caenorhabdi
885	170	9.4	291	2	Q66J15	XENTR	Q66J15	anopheles tro
886	170	9.4	300	1	JAM1	RAT	Q9JNY1	rattus norv
887	170	9.4	486	2	Q7PSS9	ANOGA	Q7PSS9	anopheles g
888	170	9.4	812	1	FGFR1	XENLA	P22182	anopheles lae
889	169.5	9.4	231	2	Q7PUU3	ANOGA	Q7PUU3	anopheles g
890	169.5	9.4	351	2	Q7SY58	BRARE	Q7SY58	brachydanio
891	169.5	9.4	351	2	Q8JFUF	BRARE	Q8JFUF	brachydanio
892	169.5	9.4	402	1	RAGE	RAT	Q63495	rattus norv
893	169.5	9.4	402	2	Q6MG86	RAT	Q6MG86	rattus norv
894	169.5	9.4	698	2	Q5TN75	ANOGA	Q5TN75	anopheles g
895	169.5	9.4	772	2	Q49AK4	HUMAN	Q49AK4	homo sapien
896	169.5	9.4	954	2	Q7PV74	ANOGA	Q7PV74	anopheles g
897	169.5	9.4	968	2	Q4W447	HORSE	Q4W447	equus cabal
898	169.5	9.4	1338	2	Q5TAR1	HUMAN	Q5TAR1	homo sapien
899	169.5	9.4	2200	2	Q7YRF6	CANFA	Q7YRF6	canis famil
900	169	9.4	368	2	Q5UB49	HUMAN	Q5UB49	homo sapien
901	169	9.4	714	2	Q4T313	TETNG	Q4T313	tetraodon n
902	169	9.4	764	1	ICCR	DROME	Q08180	drosophila
903	169	9.4	814	2	Q91897	XENLA	Q91897	anopheles lae
904	169	9.4	1254	2	Q674V1	PODCA	Q674V1	podocoryne
905	169	9.4	1378	2	Q5XNV9	PETMA	Q5XNV9	petromyzon
906	169	9.4	1415	2	Q5XNV8	PETMA	Q5XNV8	petromyzon
907	168.5	9.3	793	2	Q4RFN0	TETNG	Q4RFN0	tetraodon n

Q86LF9	drosophila	2	800	9.3	168.5	908	Q86LF9	DROVI
Q86LF8	drosophila	2	801	9.3	168.5	909	Q86LF8	DROVI
Q3UH53	mus musculus	1	2193	9.3	168.5	910	SDK1	MOUSE
Q4RE90	tetraodon n	2	7759	9.3	168.5	911	Q4RE90	TETNG
Q9VRL5	drosophila	2	215	9.3	168	912	Q9VRL5	DROME
Q9GNS	anopheles lae	2	827	9.3	168	913	Q6GNS5	XENLA
Q59EB0	homo sapien	2	1451	9.3	168	914	Q59EB0	HUMAN
Q44328	hirudo medi	2	2051	9.3	168	915	Q44328	HIRME
Q93034	carassius a	1	555	9.3	167.5	916	CD166	CARAU
Q81063	drosophila	2	784	9.3	167.5	917	Q81063	DROVI
Q9VH85	drosophila	2	939	9.3	167.5	918	Q9VH85	DROME
Q9Y619	homo sapien	2	1019	9.3	167.5	919	Q9Y619	HUMAN
Q60T65	caenorhabdi	2	1198	9.3	167.5	920	Q60T65	CAEBR
Q62230	mus musculus	1	1694	9.3	167.5	921	SN	MOUSE
Q869A0	drosophila	2	2776	9.3	167.5	922	Q869A0	DROME
Q86829	drosophila	2	2898	9.3	167.5	923	Q86829	DROME
Q7PT04	anopheles g	2	5724	9.3	167.5	924	Q7PT04	ANOGA
Q9QW78	mus sp. fib	2	376	9.2	167	925	Q9QW78	9WURI
Q8MSN7	drosophila	2	551	9.2	167	926	Q8MSN7	DROME
Q9W4T9	drosophila	2	956	9.2	167	927	Q9W4T9	DROME
Q9N9Y9	drosophila	2	959	9.2	167	928	Q9N9Y9	DROME
Q90X22	brachydanio	2	1276	9.2	167	929	Q90X22	BRARE
Q4PIU9	caenorhabdi	2	1328	9.2	167	930	Q4PIU9	CAEBL
Q35U87	caenorhabdi	2	1331	9.2	167	931	Q35U87	CAEBL
P35968	homo sapien	1	1356	9.2	167	932	VGFR2	HUMAN
Q4T2N4	tetraodon n	2	2057	9.2	167	933	Q4T2N4	TETNG
Q8Bmn8	caenorhabdi	2	2200	9.2	167	934	LAR	CAEBL
Q61GU4	caenorhabdi	2	2295	9.2	167	935	Q61GU4	CAEBR
Q5G1T4	brachydanio	2	1357	9.2	166.5	936	Q5G1T4	BRARE
Q9V7G6	drosophila	2	1506	9.2	166.5	937	Q9V7G6	DROME
Q7Z246	brachydanio	2	4039	9.2	166.5	938	Q7Z246	BRARE
Q7Q1Q0	anopheles g	2	407	9.2	166	939	Q7Q1Q0	ANOGA
Q8MYR8	drosophila	2	576	9.2	166	940	Q8MYR8	DROME
Q4SPR8	tetraodon n	2	590	9.2	166	941	Q4SPR8	TETNG
Q4T2M0	tetraodon n	2	591	9.2	166	942	Q4T2M0	TETNG
Q8TCG8	homo sapien	2	1232	9.2	166	943	Q8TCG8	HUMAN
Q9W3N2	drosophila	2	340	9.2	165.5	944	Q9W3N2	DROME
Q28939	sus scrofa	2	538	9.2	165.5	945	Q28939	PIG
Q4R603	macaca fasc	2	543	9.2	165.5	946	Q4R603	MACPA
Q9UL17	homo sapien	2	1023	9.2	165.5	947	Q9UL17	HUMAN
Q9VQW1	drosophila	2	1193	9.2	165.5	948	Q9VQW1	DROME
Q4TAD4	tetraodon n	2	3158	9.2	165.5	949	Q4TAD4	TETNG
Q4T3W5	tetraodon n	2	4648	9.2	165.5	950	Q4T3W5	TETNG
Q7PSN2	anopheles g	1	154	9.1	165	951	Q7PSN2	ANOGA
Q5TQC8	anopheles g	1	341	9.1	165	952	Q5TQC8	ANOGA
Q52KX7	anopheles lae	2	394	9.1	165	953	Q52KX7	XENLA
Q9Y3Y8	homo sapien	2	584	9.1	165	954	Q9Y3Y8	HUMAN
Q7PUM9	anopheles g	1	620	9.1	165	955	Q7PUM9	ANOGA
P16092	mus musculus	2	822	9.1	165	956	FGFR1	MOUSE
Q04589	rattus norv	1	822	9.1	165	957	FGFR1	RAT
Q60818	mus musculus	2	822	9.1	165	958	Q60818	MOUSE
Q9W4Y6	drosophila	2	998	9.1	165	959	Q9W4Y6	DROME
Q8NFA6	homo sapien	1	1014	9.1	164.5	960	Q8NFA6	HUMAN
CD166	RAT	1	583	9.1	164.5	961	CD166	RAT
Q96P30	homo sapien	1	639	9.1	164.5	962	Q96P30	HUMAN
Q96P30	homo sapien	2	822	9.1	164.5	963	Q96P30	HUMAN
Q61674	drosophila	2	822	9.1	164.5	964	Q61674	DROME
Q9V6T1	drosophila	2	822	9.1	164.5	965	Q9V6T1	DROME
Q7Q0S6	anopheles g	1	851	9.1	164.5	966	Q7Q0S6	ANOGA
Q4SK55	tetraodon n	2	1464	9.1	164.5	967	Q4SK55	TETNG
Q98D87	mus musculus	1	310	9.1	164	968	JAM3	MOUSE
Q68FQ2	rattus norv	1	310	9.1	164	969	JAM3	RAT
Q59E14	drosophila	2	465	9.1	164	970	Q59E14	DROME
Q7PXX0	anopheles g	1	628	9.1	164	971	Q7PXX0	ANOGA
Q8N612	homo sapien	2	812	9.1	164	972	Q8N612	HUMAN
Q8Cim9	mus musculus	2	820	9.1	164	973	Q8Cim9	MOUSE
Q8TAM9	homo sapien	2	924	9.1	164	974	Q8TAM9	HUMAN
Q95R27	drosophila	2	998	9.1	164	975	Q95R27	DROME
Q961K8	drosophila	2	1311	9.1	164	976	Q961K8	DROME
Q6V465	mus musculus	1	2176	9.1	164	977	SDK2	MOUSE
Q5K374	brachydanio	2	481	9.1	163.5	979	Q5K374	BRARE
Q5K373	brachydanio	2	481	9.1	163.5	980	Q5K373	BRARE

981	163.5	9.1	483	2	Q9DBP8_MOUSE	Q9dbp8 mus musculus	1054	159	8.8	2696	2	Q60WB1_CAEBR	Q60wb1 caenorhabdi
982	163.5	9.1	508	2	Q8CED8_MOUSE	Q8ced8 mus musculus	1055	158.5	8.8	211	2	Q7QBC5_ANOGA	Q7qbc5 anopheles g
983	163.5	9.1	508	2	Q8R007_MOUSE	Q8r007 mus musculus	1056	158.5	8.8	388	1	BASI_CHICK	P17790 gallus gall
984	163.5	9.1	513	2	Q9D6N4_MOUSE	Q9d6n4 mus musculus	1057	158.5	8.8	626	2	Q3TES6_MOUSE	Q3tes6 mus musculus
985	163.5	9.1	570	2	Q5R640_PONPY	Q5r640 pongo pygma	1058	158.5	8.8	683	2	Q5TTJ6_ANOGA	Q5ttj6 anopheles g
986	163.5	9.1	572	2	Q3U318_MOUSE	Q3u318 mus musculus	1059	158.5	8.8	862	2	Q4SAP3_TETNG	Q4sap3 tetraodon n
987	163.5	9.1	646	1	MUC18_HUMAN	P43121 h cell surfi	1060	158.5	8.8	912	1	ICAM5_RABIT	Q28730 oryctolagus
988	163.5	9.1	1596	2	Q9HCL6_HUMAN	Q9hcl6 homo sapien	1061	158.5	8.8	1199	2	Q21041_CAEBR	Q21041 caenorhabdi
989	163	9.0	357	2	Q18872_PIG	Q18872 sus scrofa	1062	158.5	8.8	1215	2	Q7KTI7_DROME	Q7kti7 drosophila
990	163	9.0	924	1	ICAM5_HUMAN	Q9umf0 homo sapien	1063	158.5	8.8	1278	2	Q4SW90_TETNG	Q4sw90 tetraodon n
991	163	9.0	1357	2	Q5GIT2_BRARE	Q5git2 brachydanio	1064	158.5	8.8	1461	2	Q8T9F6_DROME	Q8t9f6 drosophila
992	162.5	9.0	199	2	Q7QK35_ANOGA	Q7qk35 anopheles g	1065	158.5	8.8	1474	2	Q8T4M0_DROME	Q8t4m0 drosophila
993	162.5	9.0	332	2	Q684Q2_MOUSE	Q684q2 mus musculus	1066	158.5	8.8	1503	2	Q7KTI8_DROME	Q7kti8 drosophila
994	162.5	9.0	353	2	Q86XT3_HUMAN	Q86xt3 homo sapien	1067	158.5	8.8	1509	2	Q81PGL_DROME	Q81pgl drosophila
995	162.5	9.0	508	1	FCRL2_HUMAN	Q6glas homo sapien	1068	158.5	8.8	1509	2	Q9VLO8_DROME	Q9vlg8 drosophila
996	162.5	9.0	605	2	Q6GNL9_XENLA	Q6gnl9 xenopus lae	1069	158	8.7	286	2	Q7QC80_ANOGA	Q7qc80 anopheles g
997	162.5	9.0	628	2	Q9MZ08_BOVIN	Q9mz08 bos taurus	1070	158	8.7	302	2	Q5TPA7_ANOGA	Q5tpa7 anopheles g
998	162.5	9.0	1509	2	Q9SP10_DROME	Q9sp10 drosophila	1071	158	8.7	360	2	Q61565_MOUSE	Q61565 mus musculus
999	162.5	9.0	1535	2	Q23991_DROME	Q23991 drosophila	1072	158	8.7	361	2	Q9QW79_9MURI	Q9qw79 mus sp. fib
1000	162	9.0	385	2	Q4SQV8_TETNG	Q4sqv8 tetraodon n	1073	158	8.7	450	2	Q3LFS5_MOUSE	Q3lfs5 mus musculus
1001	162	9.0	1304	2	Q9VBES_DROSOPHILA	Q9vbes drosophila	1074	158	8.7	763	2	Q7FUH1_ANOGA	Q7fuh1 anopheles g
1002	162	9.0	4824	2	Q95YM1_PROCL	Q95ym1 procambarus	1075	158	8.7	820	2	Q53H63_HUMAN	Q53h63 homo sapien
1003	161.5	8.9	197	2	Q7PTP6_ANOGA	Q7ptp6 anopheles g	1076	158	8.7	822	2	Q9QVW7_9MURI	Q9qvww7 rattus sp.
1004	161.5	8.9	300	2	Q7PV30_ANOGA	Q7pv30 anopheles g	1077	158	8.7	977	2	Q3U3W0_MOUSE	Q3u3w0 mus musculus
1005	161.5	8.9	319	2	Q7OLK4_ANOGA	Q7olk4 anopheles g	1078	157.5	8.7	156	2	Q2LZL1_DROPS	Q2lzl1 drosophila
1006	161.5	8.9	402	2	Q9NAR0_CAEBR	Q9nar0 caenorhabdi	1079	157.5	8.7	246	2	Q9CTL3_MOUSE	Q9ctl3 mus musculus
1007	161.5	8.9	650	2	Q9GKR2_BOVIN	Q9gkr2 bos taurus	1080	157.5	8.7	441	2	Q8CL39_MOUSE	Q8cl39 mus musculus
1008	161.5	8.9	739	2	Q9GKR3_BOVIN	Q9gkr3 bos taurus	1081	157.5	8.7	496	1	MYOTI_MOUSE	Q9j1f9 mus musculus
1009	161.5	8.9	802	2	Q42127_XENLA	Q42127 xenopus lae	1082	157.5	8.7	531	2	Q7QBY7_ANOGA	Q7qby7 anopheles g
1010	161.5	8.9	2325	1	SDK_CAEBR	Q9n3x8 caenorhabdi	1083	157.5	8.7	583	1	CD166_MOUSE	Q61490 mus musculus
1011	161.5	8.9	2753	2	Q3KX34_DROME	Q3kn34 drosophila	1084	157.5	8.7	583	2	Q54AJ5_MOUSE	Q54aj5 mus musculus
1012	161.5	8.9	2935	2	Q7Z1Y4_DROME	Q7z1y4 drosophila	1085	157.5	8.7	697	1	SIG10_HUMAN	Q961c7 homo sapien
1013	161.5	8.9	2946	2	Q9W053_DROME	Q9w053 drosophila	1086	157.5	8.7	697	2	Q3MIR5_HUMAN	Q3mir5 homo sapien
1014	161	8.9	298	2	Q8INK5_DROME	Q8ink5 drosophila	1087	157.5	8.7	939	2	Q967X6_DROME	Q967x6 drosophila
1015	161	8.9	310	1	JAM3_HUMAN	Q9bx67 homo sapien	1088	157.5	8.7	939	2	Q9VB35_DROME	Q9vb35 drosophila
1016	161	8.9	336	2	Q961T8_DROME	Q961t8 drosophila	1089	157.5	8.7	978	1	KFMS_F5VMD	P00545 feline sarc
1017	161	8.9	461	2	Q13854_HUMAN	Q13854 homo sapien	1090	157.5	8.7	1376	2	Q5DTJ9_MOUSE	Q5dtj9 mus musculus
1018	161	8.9	538	2	Q29123_PIG	Q29123 sus scrofa	1091	157.5	8.7	1503	2	Q8T4L8_DROME	Q8t4l8 drosophila
1019	161	8.9	605	2	Q8TB00_HUMAN	Q8tb00 homo sapien	1092	157	8.7	298	1	JAMI_BOVIN	Q95v56 bos taurus
1020	161	8.9	693	2	Q9UPU1_HUMAN	Q9upul homo sapien	1093	157	8.7	298	2	Q5E9V8_BOVIN	Q5evx8 homo sapien
1021	161	8.9	820	2	Q5R8Q3_PONPY	Q5r8q3 pongo pygma	1094	157	8.7	299	1	JAM1_HUMAN	Q9y624 homo sapien
1022	161	8.9	1327	2	Q8QHL3_CHICK	Q8qhl3 gallus gall	1095	157	8.7	299	2	Q6FIB4_HUMAN	Q6fib4 homo sapien
1023	161	8.9	1345	2	Q8VCD0_MOUSE	Q8vcd0 mus musculus	1096	157	8.7	383	2	Q75ML9_HUMAN	Q75ml9 homo sapien
1024	161	8.9	1357	2	Q5MD89_BRARE	Q5md89 brachydanio	1097	157	8.7	446	2	Q63236_RAT	Q63236 rattus norv
1025	161	8.9	2541	2	Q19663_CAEBR	Q19663 caenorhabdi	1098	157	8.7	527	2	Q4SZU1_TETNG	Q4szul tetraodon n
1026	160.5	8.9	355	2	Q3L1R6_HUMAN	Q3l1r6 homo sapien	1099	157	8.7	641	2	Q86SD2_CIOIN	Q86sd2 ciona intes
1027	160.5	8.9	422	2	Q86CY9_HELAM	Q86cy9 helicoverpa	1100	157	8.7	707	2	Q5VXZ8_HUMAN	Q5vxz8 homo sapien
1028	160.5	8.9	646	2	Q8NHN8_HUMAN	Q8nhn8 homo sapien	1101	157	8.7	734	2	Q961A4_HUMAN	Q961a4 homo sapien
1029	160.5	8.9	980	1	CSF1R_FELCA	P13369 felis silve	1102	157	8.7	734	2	Q96P31_HUMAN	Q96p31 homo sapien
1030	160.5	8.9	1237	2	Q61OC8_CAEBR	Q61oc8 caenorhabdi	1103	157	8.7	742	2	Q8N6S2_HUMAN	Q8n6s2 brachydanio
1031	160	8.9	319	1	GPA33_HUMAN	Q99795 homo sapien	1104	157	8.7	1272	2	Q4JDD5_BRARE	Q4jdd5 caenorhabdi
1032	160	8.9	319	2	Q5VZP6_HUMAN	Q5vzp6 homo sapien	1105	157	8.7	6710	2	Q61SF4_CAEBR	Q61sf4 caenorhabdi
1033	160	8.9	491	2	Q5QNS6_BRARE	Q5qns6 brachydanio	1106	156.5	8.7	262	2	Q308M3_HUMAN	Q308m3 homo sapien
1034	160	8.9	544	2	Q7Z285_BRARE	Q7z285 brachydanio	1107	156.5	8.7	400	2	Q4T054_TETNG	Q4t054 tetraodon n
1035	160	8.9	564	1	CD166_BRARE	Q90460 brachydanio	1108	156.5	8.7	416	1	RAGE_BOVIN	Q28173 bos taurus
1036	160	8.9	564	2	Q6IQX4_BRARE	Q6iqx4 brachydanio	1109	156.5	8.7	473	2	Q5P8W7_XENLA	Q5p8w7 xenopus lae
1037	160	8.9	640	2	Q8BSM2_MOUSE	Q8bsm2 mus musculus	1110	156.5	8.7	753	2	Q5J7D9_MOUSE	Q5j7d9 mus musculus
1038	160	8.9	822	1	FGFR1_HUMAN	P11362 homo sapien	1111	156.5	8.7	797	2	Q52V39_BRAFL	Q52v39 branchiosto
1039	160	8.9	1144	2	Q18100_CAEBR	Q18100 caenorhabdi	1112	156.5	8.7	799	2	Q8C3V5_MOUSE	Q8c3v5 mus musculus
1040	160	8.9	1147	2	Q53U86_CAEBR	Q53u86 caenorhabdi	1113	156.5	8.7	799	2	Q8CIB8_MOUSE	Q8cib8 mus musculus
1041	160	8.9	1437	2	Q44329_HIRME	Q44329 hirudo medi	1114	156.5	8.7	811	2	Q9YH43_XENLA	Q9yh43 xenopus lae
1042	160	8.9	6839	2	Q23550_CAEBR	Q23550 caenorhabdi	1115	156.5	8.7	1292	2	Q4RHM3_TETNG	Q4rhm3 tetraodon n
1043	159.5	8.8	570	2	Q8NCB6_HUMAN	Q8nce6 homo sapien	1116	156	8.6	298	1	JAMI_FELCA	Q2w9k2 felis silve
1044	159.5	8.8	585	1	CEA20_HUMAN	Q6uy09 homo sapien	1117	156	8.6	551	2	Q3TAZ7_MOUSE	Q3ta27 m bf-derive
1045	159.5	8.8	975	2	Q97174_DROME	Q97174 drosophila	1118	156	8.6	692	2	Q800Y9_BRARE	Q800y9 brachydanio
1046	159	8.8	346	2	Q4PKP5_BRARE	Q4pkp5 brachydanio	1119	156	8.6	740	2	Q96P29_HUMAN	Q96p29 homo sapien
1047	159	8.8	816	2	Q91285_PLEWA	Q91285 pleurodeles	1120	156	8.6	756	2	Q800Z0_BRARE	Q800z0 brachydanio
1048	159	8.8	922	2	Q3U4N8_MOUSE	Q3u4n8 mus musculus	1121	156	8.6	945	2	Q3U1X4_MOUSE	Q3u1x4 mus musculus
1049	159	8.8	973	2	Q7QJK6_ANOGA	Q7qjk6 anopheles g	1122	156	8.6	977	1	CSF1R_MOUSE	P09581 mus musculus
1050	159	8.8	1209	2	Q4SFS8_TETNG	Q4sf88 tetraodon n	1123	156	8.6	977	2	Q3U1Y3_MOUSE	Q3u1y3 mus musculus
1051	159	8.8	1272	2	Q5GIT3_BRARE	Q5git3 brachydanio	1124	156	8.6	977	2	Q3U210_MOUSE	Q3u210 mus musculus
1052	159	8.8	1948	1	PTPRS_HUMAN	Q13332 homo sapien	1125	156	8.6	977	2	Q3U3P1_MOUSE	Q3u3p1 m nod-deriv
1053	159	8.8	2170	1	SDK2_HUMAN	Q58ex2 homo sapien	1126	156	8.6	977	2	Q3UKC6_MOUSE	Q3ukc6 mus musculus

1127	156	8.6	978	1	CSF1R_RAT	Q00495	rattus norv	1200	152	8.4	687	2	Q9JJ08_RAT	Q9JJ08	rattus norv
1128	156	8.6	1238	2	Q45S56_TETNG	Q45S56	tetraodon n	1201	152	8.4	772	2	Q5NKT7_PANTR	Q5NKT7	pan troglod
1129	156	8.6	1501	2	Q7KUK9_DROME	Q7KUK9	drosophila	1202	152	8.4	783	2	Q86T42_HUMAN	Q86T42	homo sapien
1130	156	8.6	7158	2	Q23551_CABEL	Q23551	caenorhabdi	1203	152	8.4	880	1	TYRO3_RAT	TYRO3	rattus norv
1131	155.5	8.6	761	2	Q95LQ2_BACFL	Q95LQ2	macaca fasc	1204	152	8.4	1024	2	Q63HJ3_HUMAN	Q63HJ3	homo sapien
1132	155.5	8.6	797	2	Q52V40_BRACFL	Q52V40	branchiost	1205	152	8.4	1123	2	Q569K7_HUMAN	Q569K7	homo sapien
1133	155.5	8.6	880	1	TYRO3_MOUSE	P55144	mus musculus	1206	152	8.4	1141	1	MYPC1_HUMAN	MYPC1	homo sapien
1134	155.5	8.6	880	2	Q6NZM6_MOUSE	Q6NZM6	mus musculus	1207	152	8.4	1148	2	Q86T39_HUMAN	Q86T39	homo sapien
1135	155	8.6	226	2	Q4DM1_TETNG	Q4dm1	tetraodon n	1208	152	8.4	1148	2	Q8N3L2_HUMAN	Q8N3L2	homo sapien
1136	155	8.6	299	2	Q2WKK1_CERAE	Q2wkk1	cercopithec	1209	152	8.4	1148	2	Q8N3R4_HUMAN	Q8N3R4	homo sapien
1137	155	8.6	373	2	Q9H6B4_HUMAN	Q9H6B4	homo sapien	1210	152	8.4	1171	2	Q86TA8_HUMAN	Q86TA8	homo sapien
1138	155	8.6	454	2	Q91W54_MOUSE	Q91W54	mus musculus	1211	152	8.4	1171	2	Q86TC8_HUMAN	Q86TC8	homo sapien
1139	155	8.6	458	2	Q61351_MOUSE	Q61351	mus musculus	1212	152	8.4	1343	1	VGFR2_RAT	VGFR2	rattus norv
1140	155	8.6	521	1	CEAM1_MOUSE	P31809	mus musculus	1213	152	8.4	1363	1	VGFR3_RAT	VGFR3	rattus norv
1141	155	8.6	521	2	Q61352_MOUSE	Q61352	mus musculus	1214	151.5	8.4	344	1	CEAM6_HUMAN	CEAM6	homo sapien
1142	155	8.6	521	2	Q925P3_MOUSE	Q925P3	mus musculus	1215	151.5	8.4	344	2	Q13774_HUMAN	Q13774	homo sapien
1143	155	8.6	540	2	Q4RT9_TETNG	Q4rt9	tetraodon n	1216	151.5	8.4	344	2	Q53XP7_HUMAN	Q53XP7	homo sapien
1144	155	8.6	677	2	Q7PWJ1_ANOGA	Q7PWj1	anopheles g	1217	151.5	8.4	459	2	Q4RS41_TETNG	Q4RS41	tetraodon n
1145	155	8.6	699	2	Q4RT82_TETNG	Q4rt82	tetraodon n	1218	151.5	8.4	564	2	Q7ZU00_BRARE	Q7ZU00	brachydanio
1146	155	8.6	819	1	FGPR1_CHICK	P21804	gallus gall	1219	151.5	8.4	847	1	FSTL5_MOUSE	FSTL5	mouse
1147	155	8.6	851	2	Q2XUS3_HUMAN	Q2xus3	homo sapien	1220	151.5	8.4	847	2	Q3UUI4_MOUSE	Q3UUI4	mus musculus
1148	155	8.6	977	1	FCRL5_HUMAN	Q6rdr9	homo sapien	1221	151.5	8.4	948	2	Q9TUD7_TRIVU	Q9TUD7	trichosurus
1149	155	8.6	998	2	Q495Q3_HUMAN	Q495q3	homo sapien	1222	151.5	8.4	1898	2	Q9EQ17_MOUSE	Q9EQ17	mus musculus
1150	155	8.6	1343	2	Q5PQU0_RAT	P35917	rattus norv	1223	151	8.4	402	2	Q5UE88_CABEL	Q5UE88	caenorhabdi
1151	155	8.6	1363	1	VGPR3_MOUSE	P35917	mus musculus	1224	151	8.4	413	2	Q699P0_ANTPE	Q699P0	antheraea p
1152	155	8.6	1363	2	Q5SU94_MOUSE	Q5su94	mus musculus	1225	151	8.4	497	2	Q4RFP7_TETNG	Q4RFP7	tetraodon n
1153	155	8.6	1367	1	VGPR2_MOUSE	P35918	mus musculus	1226	151	8.4	814	2	Q59H40_HUMAN	Q59H40	homo sapien
1154	154.5	8.6	257	2	Q4S0M3_TETNG	Q4S0m3	tetraodon n	1227	151	8.4	1156	2	Q676C3_PUROC	Q676C3	oikopleura
1155	154.5	8.6	602	1	NRG1_CHICK	Q05199	gallus gall	1228	150.5	8.3	1367	2	Q7PQP4_ANOGA	Q7PQP4	anopheles g
1156	154.5	8.6	1387	2	Q4SJQ3_TETNG	Q4sjq3	tetraodon n	1229	150.5	8.3	208	2	Q4RK89_TETNG	Q4RK89	tetraodon n
1157	154.5	8.6	1897	1	PTPRF_HUMAN	P10586	homo sapien	1230	150.5	8.3	417	2	Q4S916_TETNG	Q4S916	tetraodon n
1158	154.5	8.6	1898	2	Q8W021_HUMAN	Q5t021	homo sapien	1231	150.5	8.3	437	2	Q8NF56_HUMAN	Q8NF56	homo sapien
1159	154.5	8.6	1898	2	Q8W8S0_HUMAN	Q8w8s0	homo sapien	1232	150.5	8.3	509	2	Q91YK7_MOUSE	Q91YK7	mus musculus
1160	154.5	8.6	1907	2	Q5T0G2_HUMAN	Q5t0g2	homo sapien	1233	150.5	8.3	510	2	Q96NY8_HUMAN	Q96NY8	homo sapien
1161	154.5	8.6	1918	2	Q5W9G2_HUMAN	Q5w9g2	homo sapien	1234	150.5	8.3	510	2	Q96K15_HUMAN	Q96K15	homo sapien
1162	154.5	8.6	2095	2	Q4RYE5_TETNG	Q4rye5	tetraodon n	1235	150.5	8.3	739	2	Q60NV9_CAEHR	Q60NV9	caenorhabdi
1163	154	8.5	624	2	Q9ESS6_RAT	Q9ess6	rattus norv	1236	150.5	8.3	747	2	Q5DT24_MOUSE	Q5DT24	mus musculus
1164	154	8.5	648	1	IRCL18_MOUSE	Q8r2y2	mus musculus	1237	150.5	8.3	824	2	Q90749_CHICK	Q90749	gallus gall
1165	154	8.5	686	1	IRPL2_HUMAN	Q9np60	h x-linked	1238	150.5	8.3	875	2	Q4RKX6_TETNG	Q4RKX6	tetraodon n
1166	154	8.5	686	2	Q5H9L9_HUMAN	Q5h9l9	homo sapien	1239	150.5	8.3	888	2	Q7ZWM9_XENLA	Q7ZWM9	xenopus lae
1167	154	8.5	816	2	Q86PM4_HYDAT	Q86pm4	hydra atten	1240	150.5	8.3	961	1	ROBO4_RAT	ROBO4	rattus norv
1168	154	8.5	1348	1	VGPR2_COTJA	P52583	coturnix co	1241	150.5	8.3	1047	2	Q4RGCT_TETNG	Q4RGCT	tetraodon n
1169	154	8.5	1919	2	Q7OCPO_ANOGA	Q7ocp0	anopheles g	1242	150.5	8.3	1065	2	Q4RH24_TETNG	Q4RH24	tetraodon n
1170	153.5	8.5	123	2	Q7OBV1_ANOGA	Q7obv1	anopheles g	1243	150.5	8.3	1298	1	VGFR3_HUMAN	VGFR3	homo sapien
1171	153.5	8.5	226	2	Q4T419_TETNG	Q4t419	tetraodon n	1244	150.5	8.3	1298	2	Q86W08_HUMAN	Q86W08	homo sapien
1172	153.5	8.5	280	2	Q93350_CABEL	Q93350	caenorhabdi	1245	150.5	8.3	1363	2	Q86W07_HUMAN	Q86W07	homo sapien
1173	153.5	8.5	510	2	Q5E929_BOVIN	Q5e929	bos taurus	1246	150.5	8.3	1478	2	Q59H90_HUMAN	Q59H90	homo sapien
1174	153.5	8.5	1173	2	Q6NR54_DROME	Q6nr54	drosophila	1247	150.5	8.3	296	2	Q59DX6_DROME	Q59DX6	homo sapien
1175	153.5	8.5	1905	2	Q5VVL9_HUMAN	Q5vvl9	homo sapien	1248	150	8.3	323	2	Q5U198_DROME	Q5U198	drosophila
1176	153.5	8.5	2177	1	SDK2_CHICK	Q8av57	gallus gall	1249	150	8.3	343	2	Q7TP22_RAT	Q7TP22	rattus norv
1177	153.5	8.5	6048	2	Q7JN85_CABEL	Q7jn85	caenorhabdi	1250	150	8.3	366	1	IRPL2_MOUSE	IRPL2	mus musculus
1178	153	8.5	686	2	Q7PQM9_ANOGA	Q7pqm9	anopheles g	1251	150	8.3	686	1	Q24205_DROME	Q24205	drosophila
1179	153	8.5	870	2	Q7PYG1_ANOGA	Q7pyg1	anopheles g	1252	150	8.3	711	2	Q6NXV8_MOUSE	Q6NXV8	mus musculus
1180	153	8.5	1108	2	Q5RJH4_MOUSE	Q5rjh4	mus musculus	1253	150	8.3	977	2	Q86T48_HUMAN	Q86T48	homo sapien
1181	153	8.5	1348	2	Q677M1_CHICK	Q677m1	gallus gall	1254	150	8.3	1171	2	Q7PSS8_ANOGA	Q7PSS8	anopheles g
1182	153	8.5	1505	2	Q3KPJ0_HUMAN	Q3kpj0	homo sapien	1255	149.5	8.3	173	2	Q7PUC4_ANOGA	Q7PUC4	anopheles g
1183	153	8.5	1506	2	Q3KPJ1_HUMAN	Q3kpj1	homo sapien	1256	149.5	8.3	211	2	Q45U77_CAEHR	Q45U77	caenorhabdi
1184	153	8.5	1788	2	Q91AJ0_XENLA	Q91aj0	xenopus lae	1257	149.5	8.3	261	2	Q8BJ10_MOUSE	Q8BJ10	mus musculus
1185	153	8.5	1912	1	PTPRD_HUMAN	P23468	homo sapien	1258	149.5	8.3	349	1	CEAM8_HUMAN	CEAM8	homo sapien
1186	152.5	8.4	347	2	Q6PJS2_HUMAN	Q6pis2	homo sapien	1259	149.5	8.3	360	2	Q8BJ10_MOUSE	Q8BJ10	mus musculus
1187	152.5	8.4	509	2	Q9FQY5_MOUSE	Q9fqy5	m mman-g pr	1260	149.5	8.3	739	1	VCAM1_RAT	VCAM1	rattus norv
1188	152.5	8.4	519	1	CEAM1_RAT	P15573	rattus norv	1261	149.5	8.3	739	2	Q5FV53_RAT	Q5FV53	brachydanio
1189	152.5	8.4	1484	2	Q5W9G3_HUMAN	Q5w9g3	homo sapien	1262	149.5	8.3	815	2	Q805B9_BRARE	Q805B9	brachydanio
1190	152.5	8.4	1802	2	Q28633_RABIT	Q28633	oryctolagus	1263	149.5	8.3	854	2	Q4ACB3_BRARE	Q4ACB3	brachydanio
1191	152.5	8.4	2290	2	Q4S6A6_TETNG	Q4s6a6	tetraodon n	1264	149.5	8.3	1073	2	Q9W1T8_DROME	Q9W1T8	drosophila
1192	152.5	8.4	6225	2	Q7PUM6_ANOGA	Q7pum6	anopheles g	1265	149.5	8.3	1250	2	Q8TDY8_HUMAN	Q8TDY8	homo sapien
1193	152	8.4	160	2	Q3KZB1_SCHJA	Q3kzb1	schistosoma	1266	149.5	8.3	1501	2	Q4JFL8_RAT	Q4JFL8	rattus norv
1194	152	8.4	369	2	Q5VU70_RAT	Q5vj70	rattus norv	1267	149.5	8.3	1501	2	Q9QW00_9MURI	Q9QW00	rattus sp.
1195	152	8.4	476	2	Q4R4S1_MACFA	Q4r4s1	macaca fasc	1268	149.5	8.3	1863	2	Q64605_RAT	Q64605	rattus norv
1196	152	8.4	617	2	Q5MY54_BRACHYDANIO	Q5my54	brachydanio	1269	149.5	8.3	1907	2	Q3KRE9_RAT	Q3KRE9	rattus norv
1197	152	8.4	617	2	Q5IF12_BRARE	Q5ifi2	brachydanio	1270	149	8.3	335	2	Q75237_HUMAN	Q75237	homo sapien
1198	152	8.4	620	2	Q4S1C0_TETNG	Q4s1c0	tetraodon n	1271	149	8.3	372	2	Q8K1G0_RAT	Q8K1G0	rattus norv
1199	152	8.4	636	2	Q22040_CABEL	Q22040	caenorhabdi	1272	149	8.3	373	2	Q8R373_MOUSE	Q8R373	mus musculus

1273	149	8.3	388	2	Q9Z151_MOUSE	Q9Z151 mus musculus	1346	145.5	8.1	188	2	O5SZJ1_HUMAN	Q5SZJ1 homo sapien
1274	149	8.3	483	2	Q4RRX0_TETNG	Q4rrx0 tetraodon n	1347	145.5	8.1	292	2	O6S172_BRARE	O6S172 brachydanio
1275	149	8.3	570	2	Q6GLY1_XENLA	Q6gly1 xenopus lae	1348	145.5	8.1	391	2	O4S871_TETNG	O4S871 tetraodon n
1276	149	8.3	1276	2	Q4SFF7_TETNG	Q4sff7 tetraodon n	1349	145.5	8.1	504	2	Q6NNAI_DROME	Q6nnai drosophila
1277	149	8.3	1894	1	PTPRD_MOUSE	Q64487 mus musculus	1350	145.5	8.1	508	2	Q9VGD2_DROME	Q9vgd2 mus musculus
1278	148.5	8.2	248	2	Q3TQ52_MOUSE	Q3tq52 mus musculus	1351	145.5	8.1	520	2	Q925P2_MOUSE	Q925p2 mus musculus
1279	148.5	8.2	260	2	Q4S828_TETNG	O4s828 tetraodon n	1352	145.5	8.1	664	2	Q9VGD3_DROME	Q9vgd3 drosophila
1280	148.5	8.2	289	2	Q7ZWTO_XENLA	Q7zwt0 xenopus lae	1353	145.5	8.1	713	2	Q4S6E0_TETNG	O4s6e0 tetraodon n
1281	148.5	8.2	476	2	Q7ZXU8_XENLA	Q7zxj8 xenopus lae	1354	145.5	8.1	739	1	VCAM1_MOUSE	P29533 mus musculus
1282	148.5	8.2	521	1	CD166_CANFA	O46634 canis famill	1355	145.5	8.1	739	2	Q3TR98_MOUSE	Q3tr98 mus musculus
1283	148.5	8.2	536	2	Q9GV82_DROME	O9gv82 drosophila	1356	145.5	8.1	739	2	Q3UPN1_MOUSE	Q3upn1 mus musculus
1284	148.5	8.2	574	1	PVRL3_BRARE	O58eq3 brachydanio	1357	145.5	8.1	739	2	Q91X98_MOUSE	Q91x98 mus musculus
1285	148.5	8.2	588	1	CD166_CHICK	P42292 gallus gall	1358	145.5	8.1	808	1	Q9FR4_MOUSE	O9fr4 mus musculus
1286	148.5	8.2	673	2	Q6MZW2_HUMAN	Q6mzw2 homo sapien	1359	145.5	8.1	831	2	Q71SV9_CHICK	O71sv9 gallus gall
1287	148.5	8.2	821	2	Q9YH44_XENLA	Q9yh44 xenopus lae	1360	145.5	8.1	1012	1	ROBO4_MOUSE	O8c310 mus musculus
1288	148.5	8.2	1173	2	Q9VJ78_DROME	Q9vj78 drosophila	1361	145.5	8.1	1898	2	O64604_RAT	O64604 rattus norv
1289	148.5	8.2	1192	2	O61084_CAEBR	Q61084 caenorhabdi	1362	145.5	8.1	6101	2	Q7FXW9_ANOGA	O7fxw9 anopheles g
1290	148.5	8.2	1497	2	O5XJV4_MOUSE	O5xjv4 mus musculus	1363	145.5	8.1	241	2	Q4T4Z6_TETNG	O4t4z6 tetraodon n
1291	148.5	8.2	1501	2	Q2M3P7_HUMAN	O2m3r7 homo sapien	1364	145.5	8.0	259	2	Q9V5B2_HUMAN	Q9v5b2 homo sapien
1292	148.5	8.2	1501	2	Q7TT17_MOUSE	Q7tt17 mus musculus	1365	145.5	8.0	362	2	Q4T2X1_TETNG	O4t2x1 tetraodon n
1293	148.5	8.2	1502	2	Q9UM81_HUMAN	Q9um81 homo sapien	1366	145.5	8.0	373	2	Q920S5_MOUSE	Q920s5 mus musculus
1294	148.5	8.2	1560	2	Q95FX6_HUMAN	Q95fx6 homo sapien	1367	145.5	8.0	622	2	Q9ESS5_MOUSE	Q9ess5 mus musculus
1295	148.5	8.2	1887	2	Q9QW67_SMURI	Q9qw67 rattus sp.	1368	145.5	8.0	725	2	Q59HE0_HUMAN	O59he0 homo sapien
1296	148.5	8.2	1904	2	O64699_MOUSE	O64699 mus musculus	1369	145.5	8.0	782	2	Q9TT23_RABIT	O9tt23 oryctolagus
1297	148.5	8.2	1907	2	Q4JFC7_MOUSE	O4jfc7 mus musculus	1370	145.5	8.0	812	2	O8MZ57_DROME	O8mz57 drosophila
1298	148	8.2	507	2	Q3UQZ6_MOUSE	Q3uqz6 mus musculus	1371	145.5	8.0	878	2	Q9GV22_MYGA	O9gv22 mytilus gal
1299	148	8.2	622	2	Q9JKB2_MOUSE	Q9jkb2 mus musculus	1372	145.5	8.0	949	2	Q4RHT4_TETNG	O4rht4 tetraodon n
1300	148	8.2	694	2	Q8SMT7_DROME	Q8swt7 drosophila	1373	145.5	8.0	972	1	CSF1R_HUMAN	P07333 homo sapien
1301	148	8.2	709	2	O8IXC7_HUMAN	O8ixc7 homo sapien	1374	145.5	8.0	972	2	O86VW7_HUMAN	O86vw7 homo sapien
1302	148	8.2	821	2	O4S2G2_TETNG	O4s2g2 tetraodon n	1375	145.5	8.0	1389	2	Q4VA61_MOUSE	O4va61 mus musculus
1303	148	8.2	901	2	Q4SBD4_TETNG	O4sbd4 tetraodon n	1376	144.5	8.0	421	2	Q9NBB2_DROME	O9nbb2 drosophila
1304	148	8.2	1496	2	Q3KPI9_HUMAN	Q3kpi9 homo sapien	1377	144.5	8.0	559	2	Q7PSH7_ANOGA	O7psh7 anopheles g
1305	148	8.2	1505	2	Q3KPJ2_HUMAN	Q3kpi2 homo sapien	1378	144.5	8.0	648	1	MUC1L_RAT	O8k0x1 mus musculus
1306	147.5	8.2	318	2	Q91664_XENLA	Q91664 xenopus lae	1379	144.5	8.0	739	2	O8BZ76_MOUSE	O8bz76 m adult mal
1307	147.5	8.2	331	2	Q63239_RAT	Q63239 rattus norv	1380	144.5	8.0	754	2	Q8QFP9_XENLA	O8qfp9 xenopus lae
1308	147.5	8.2	403	1	RAGE_MOUSE	O62151 mus musculus	1381	144.5	8.0	880	2	O4JFL6_RAT	O4jfl6 rattus norv
1309	147.5	8.2	446	2	Q63237_RAT	Q63237 rattus norv	1382	144.5	8.0	1261	2	Q4JFL7_RAT	O4jfl7 rattus norv
1310	147.5	8.2	495	2	Q3UT02_MOUSE	Q3utu2 mus musculus	1383	144.5	8.0	1495	2	Q4RE88_TETNG	O4re88 tetraodon n
1311	147.5	8.2	573	2	Q6GN50_XENLA	Q6gn50 xenopus lae	1384	144.5	8.0	3084	2	Q9QYL3_MOUSE	Q9qyl3 mus musculus
1312	147.5	8.2	817	2	Q4H2M8_CIOIN	Q4h2m8 ciona intes	1385	144.5	8.0	278	2	Q6ZNI1_HUMAN	O6zni1 homo sapien
1313	147.5	8.2	824	2	Q4ACB2_BRARE	O4acb2 brachydanio	1386	144.5	8.0	413	2	O6ZNR61_LYMDI	O6znr61 lymantria d
1314	147.5	8.2	1499	2	Q90815_CHICK	Q90815 gallus gall	1387	144.5	8.0	422	2	O6WR61_HUMAN	O6wr61 homo sapien
1315	147.5	8.2	4194	2	O61S53_CAEBR	O61s53 caenorhabdi	1388	144.5	8.0	434	2	O6DN72_HUMAN	O6dn72 homo sapien
1316	147	8.1	262	2	Q5U9P8_FLOIN	Q5u9p8 plodia inte	1389	144.5	8.0	444	2	O5ZTA8_CHICK	O5zia8 gallus gall
1317	147	8.1	402	2	Q35444_MOUSE	Q35444 mus musculus	1390	144.5	8.0	542	2	Q8NHN5_HUMAN	O8nhn5 homo sapien
1318	147	8.1	549	1	PVRL3_BOVIN	Q9nq33 homo sapien	1391	144.5	8.0	891	2	Q2S177_HYDAT	Q2s177 hydra atten
1319	147	8.1	739	1	PECAL1_HUMAN	P51866 bos taurus	1392	143.5	7.9	291	2	Q2VPP6_XENLA	Q2vpp6 xenopus lae
1320	147	8.1	1044	2	Q96IW3_HUMAN	Q96iw3 homo sapien	1393	143.5	7.9	296	2	Q640C0_XENLA	O640c0 xenopus lae
1321	147	8.1	1237	2	Q75147_HUMAN	Q75147 homo sapien	1394	143.5	7.9	300	2	Q7SYQ7_XENLA	O7syq7 xenopus lae
1322	147	8.1	1252	2	Q9JL11_MOUSE	Q9jll1 mus musculus	1395	143.5	7.9	430	2	O8N4F1_HUMAN	O8n4f1 homo sapien
1323	146.5	8.1	291	2	Q65807_HUMAN	Q658q7 homo sapien	1396	143.5	7.9	556	2	Q4SFP7_TETNG	O4sfp7 tetraodon n
1324	146.5	8.1	326	2	Q8NC17_HUMAN	Q8nc17 homo sapien	1397	143.5	7.9	1177	2	Q21391_CABEL	Q21391 caenorhabdi
1325	146.5	8.1	468	2	Q9XY08_BOMMO	Q9xy08 bombyx mori	1398	143.5	7.9	12268	2	Q8MQ08_CABEL	O8mq08 caenorhabdi
1326	146.5	8.1	484	2	Q9YJ08_MOUSE	Q9yj08 mus musculus	1399	143.5	7.9	13100	2	O9165_CABEL	O9165 caenorhabdi
1327	146.5	8.1	847	1	F5TL5_HUMAN	O8n475 homo sapien	1400	143.5	7.9	310	2	O4V8T3_BRARE	O4v8t3 brachydanio
1328	146.5	8.1	1111	2	Q8BJ14_BRARE	Q8bj14 brachydanio	1401	143.5	7.9	442	2	O8C306_MOUSE	O8c306 mus musculus
1329	146.5	8.1	1280	2	Q9EPJ2_MOUSE	Q9epj2 mus musculus	1402	143.5	7.9	620	1	SME_COTJA	Q22154 coturnix co
1330	146.5	8.1	1303	2	Q5SPJ6_MOUSE	Q5spj6 bos taurus	1403	143.5	7.9	688	2	O55095_MOUSE	O55095 mus musculus
1331	146	8.1	304	2	Q3MHW8_BOVIN	Q3mhw8 bos taurus	1404	143.5	7.9	688	2	Q3TJC1_MOUSE	Q3tjc1 mus musculus
1332	146	8.1	334	2	Q2PGG1_MOUSE	Q2pgg1 mus musculus	1405	143.5	7.9	688	2	O8K1H4_MOUSE	O8k1h4 mus musculus
1333	146	8.1	486	2	Q8CGH8_MOUSE	Q8cgh8 mus musculus	1406	143.5	7.9	972	2	O761I0_CALJA	O761i0 callithrix
1334	146	8.1	549	1	PVRL3_MOUSE	Q9j169 mus musculus	1407	143.5	7.9	977	2	Q918N6_BRARE	O918n6 brachydanio
1335	146	8.1	782	2	P79390_BOSPR	P79390 bos primige	1408	143.5	7.9	1011	2	Q24273_DROME	Q24273 drosophila
1336	146	8.1	738	2	Q61563_MOUSE	Q61563 mus musculus	1409	143.5	7.9	1087	2	Q9VNP2_DROME	Q9vnp2 drosophila
1337	146	8.1	790	2	O8C4N3_MOUSE	O8c4n3 mus musculus	1410	142.5	7.9	218	2	O7Q385_ANOGA	O7q385 anopheles g
1338	146	8.1	827	1	NTRK3_CHICK	Q91044 gallus gall	1411	142.5	7.9	324	2	Q8NBY8_HUMAN	Q8nby8 homo sapien
1339	146	8.1	867	2	Q59DZ1_DROME	Q59dz1 drosophila	1412	142.5	7.9	326	2	Q9UPK8_HUMAN	Q9upk8 homo sapien
1340	146	8.1	1087	2	Q7ZY71_XENLA	Q7zy71 xenopus lae	1413	142.5	7.9	435	1	PSG6_HUMAN	Q00889 homo sapien
1341	146	8.1	1088	1	PGFRA_RAT	P20786 rattus norv	1414	142.5	7.9	461	2	QSR1V2_BRARE	O5riv2 brachydanio
1342	146	8.1	1089	1	PGFRA_MOUSE	P26618 mus musculus	1415	142.5	7.9	515	2	Q4GRE0_HUMAN	Q4gre0 homo sapien
1343	146	8.1	1089	2	Q3TQ37_MOUSE	Q3tq37 mus musculus	1416	142.5	7.9	530	2	Q4RTW9_TETNG	O4rtw9 tetraodon n
1344	146	8.1	1089	2	Q7TSJ3_MOUSE	O7tsj3 m pdgfra pr	1417	142.5	7.9	739	1	VCAM1_HUMAN	P19320 homo sapien
1345	146	8.1	1196	2	Q3V1M1_MOUSE	Q3v1m1 mus musculus	1418	142.5	7.9	739	2	Q5R847_PONPY	O5r847 pongo pygma

1419	142.5	7.9	956	1	UNC5D_MOUSE	Q8kl82	mus musculus
1420	142.5	7.9	1019	2	Q8UVR8_FUGRU	Q8uvr8	figu rubrip
1421	142.5	7.9	1052	1	FGFR2_DROME	Q09147	drosophila
1422	142	7.9	344	2	Q8WR43_CABEL	Q8wr42	caenorhabdi
1423	142	7.9	345	2	Q8MPV0_CABEL	Q8mpv0	caenorhabdi
1424	142	7.9	494	2	Q9ESC6_MOUSE	Q9esc6	mus musculus
1425	142	7.9	505	2	Q9U965_GROCY	Q9u965	geodia cydo
1426	142	7.9	806	1	CEK2_CHICK	P18460	gallus gall
1427	142	7.9	1252	2	Q9EQS9_MOUSE	Q9eqs9	mus musculus
1428	142	7.9	1253	2	Q9EQS8_MOUSE	Q9eqs8	mus musculus
1429	142	7.9	2322	1	SDK_CABER	Q60zn5	caenorhabdi
1430	141.5	7.8	324	2	Q9UPK9_HUMAN	Q9upk9	homo sapien
1431	141.5	7.8	333	2	Q75238_HUMAN	Q75238	homo sapien
1432	141.5	7.8	881	1	Q965M2_CABEL	Q965m2	caenorhabdi
1433	141.5	7.8	953	1	UNC5D_HUMAN	Q6ux24	homo sapien
1434	141.5	7.8	1007	1	ROBO4_HUMAN	Q8wz75	homo sapien
1435	141.5	7.8	1227	2	Q21038_CABEL	Q21038	caenorhabdi
1436	141.5	7.8	2000	2	Q97791_RABIT	Q97791	oryctolagus
1437	141	7.8	276	2	Q6P0R7_BRARE	Q6p0r7	brachydanio
1438	141	7.8	303	2	Q4SF99_TETNG	Q4sf99	tetradodon n
1439	141	7.8	308	2	Q503N7_BRARE	Q503n7	brachydanio
1440	141	7.8	338	2	Q6DHD4_BRARE	Q6dhd4	brachydanio
1441	141	7.8	356	2	Q59DZ4_DROME	Q59dza	drosophila
1442	141	7.8	432	2	Q6DDE7_XENLA	Q6dde7	xenopus lae
1443	141	7.8	626	2	Q6DCH3_XENLA	Q6dch3	xenopus lae
1444	141	7.8	801	2	Q3UPE1_MOUSE	Q3upe1	mus musculus
1445	141	7.8	815	2	Q8AYP3_BRARE	Q8ayp3	brachydanio
1446	141	7.8	819	2	Q4T5K0_TETNG	Q4t5k0	tetradodon n
1447	141	7.8	821	1	FGFR2_HUMAN	P21802	homo sapien
1448	141	7.8	879	2	Q8VI99_RAT	Q8vi99	rattus norv
1449	141	7.8	888	2	Q8VIA0_HUMAN	Q8via0	rattus norv
1450	141	7.8	977	2	Q98SUI_9TELE	Q98sui	danio nigro
1451	140.5	7.8	390	2	Q4S8T4_TETNG	Q4s8t4	tetradodon n
1452	140.5	7.8	413	2	Q4HIG8_SAMCR	Q4hig8	samia cynch
1453	140.5	7.8	705	2	Q63710_RATRT	Q63710	rattus norv
1454	140.5	7.8	737	2	Q965M3_CABEL	Q965m3	caenorhabdi
1455	140.5	7.8	743	2	Q6P4H5_HUMAN	Q6p4h5	homo sapien
1456	140.5	7.8	790	2	Q90699_CHICK	Q90699	gallus gall
1457	140.5	7.8	823	1	CEK3_CHICK	P18461	gallus gall
1458	140.5	7.8	1007	2	Q2XWP6_BOTSH	Q2xwp6	botryllus s
1459	140.5	7.8	1049	2	Q4S0F2_TETNG	Q4s0f2	tetradodon n
1460	140.5	7.8	1079	2	Q657G6_CANFA	Q667g6	canis famli
1461	140.5	7.8	1089	1	PGFRA_HUMAN	P16234	homo sapien
1462	140.5	7.8	2164	2	Q91AR9_CHICK	Q91ar9	gallus gall
1463	140	7.8	287	2	Q7Q894_ANOGA	Q7q894	anopheles g
1464	140	7.8	562	2	Q6YNR7_BRARE	Q6ynr7	brachydanio
1465	140	7.8	622	2	Q9R069_MOUSE	Q9r069	mus musculus
1466	140	7.8	650	2	Q9XK86_MOUSE	Q9xk86	mus musculus
1467	140	7.8	752	2	Q9XYS4_HYDAT	Q9xys4	hydra atten
1468	140	7.8	762	2	Q3TQL1_MOUSE	Q3tql1	mus musculus
1469	140	7.8	800	2	Q7TSI8_MOUSE	Q7tsi8	mus musculus
1470	140	7.8	800	2	Q99052_MOUSE	Q99052	mus musculus
1471	140	7.8	800	2	Q918X3_BRARE	Q918x3	brachydanio
1472	140	7.8	801	1	FGFR3_MOUSE	Q61851	mus musculus
1473	140	7.8	879	1	FRP3_HUMAN	Q9p2b2	homo sapien
1474	140	7.8	879	2	Q5VVU9_HUMAN	Q5vvu9	homo sapien
1475	140	7.8	890	1	TRO3_HUMAN	Q06418	homo sapien
1476	140	7.8	890	2	Q86VR3_HUMAN	Q86vr3	homo sapien
1477	140	7.8	951	2	Q59FM9_HUMAN	Q59fm9	homo sapien
1478	140	7.8	972	2	Q99662_HUMAN	Q99662	homo sapien
1479	140	7.8	976	1	KIT_HUMAN	P10721	homo sapien
1480	140	7.8	976	2	Q61Q28_HUMAN	Q61q28	homo sapien
1481	140	7.8	2888	2	Q8MMK1_BOMMO	Q8mmk1	bombux mori
1482	140	7.8	3239	2	Q8T102_BOMMO	Q8t102	bombux mori
1483	140	7.8	4203	2	Q965G2_CABEL	Q965g2	caenorhabdi
1484	140	7.8	4219	2	Q9NL87_CABEL	Q9nl87	caenorhabdi
1485	140	7.8	4250	2	Q5PY59_CABEL	Q5py59	caenorhabdi
1486	140	7.8	4369	2	Q8MXD7_CABEL	Q8mxd7	caenorhabdi
1487	140	7.8	4447	2	Q8MXD8_CABEL	Q8mxd8	caenorhabdi
1488	140	7.8	4889	2	Q9TXK2_CABEL	P11462	caenorhabdi
1489	139.5	7.7	419	1	PSG1_HUMAN	P11462	homo sapien
1490	139.5	7.7	422	2	Q96PJ3_HUMAN	Q96pj3	homo sapien
1491	139.5	7.7	431	2	Q5DX21_HUMAN	Q5dx21	homo sapien

1492	139.5	7.7	515	2	Q96PJ5_HUMAN	Q96pj5	homo sapien
1493	139.5	7.7	544	2	Q7ZY97_XENLA	Q7zy97	xenopus lae
1494	139.5	7.7	670	2	Q7ZZ47_BRARE	Q7zz47	brachydanio
1495	139.5	7.7	696	2	Q5DU03_MOUSE	Q5du03	mus musculus
1496	139.5	7.7	739	1	VCAMI_CANFA	Q28260	canis famli
1497	139.5	7.7	739	2	Q53FL7_HUMAN	Q53fl7	homo sapien
1498	139.5	7.7	743	2	Q6P1M7_HUMAN	Q6p1m7	homo sapien
1499	139.5	7.7	821	1	FGFR2_MOUSE	P21803	mus musculus
1500	139.5	7.7	829	2	Q5TZ34_BRARE	Q5tz34	brachydanio

ALIGNMENTS

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Q5R554_PONPY PRELIMINARY; PRT; 344 AA.
ID Q5R554_PONPY
AC Q5R554;
DT 21-DEC-2004, integrated into UniProtKB/TrEMBL.
DT 21-DEC-2004, sequence version 1.
DE 21-FEB-2006, entry version 11.
DE Hypothetical protein DKFZp459A2018.
GN Name=DKFZp459A2018;
OS Pongo pygmaeus (Orangutan).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Pongo.
OX NCBI_TaxID=9600;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Cortex;
RG The German cDNA Consortium;
RA Koehrer K., Beyer A., Mewes H.W., Weil B., Amid C., Osanger A.,
FOBO G., Han M., Wicmann S.; to the EMBL/GenBank/DBJ databases.
RL Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor (By similarity).
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC EMBL; CR861018; CAH93112.1; -; mRNA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005923; C:tight junction; IEA.
DR GO; GO:0005515; F:protein binding; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR013098; I-set.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG_c2.
DR InterPro; IPR013151; Immunoglobulin.
DR SMART; SM00409; IG; 3.
DR SMART; SM00408; IGE2; 2.
DR PROSITE; PS00835; IG_LIKE; 3.
KW Cell adhesion; Hypothetical protein; Immunoglobulin domain; Membrane;
KW Repeat; Tight junction.
SQ SEQUENCE 344 AA; 37998 MW; E766F4777B31D288 CRC64;

Query Match 99.5%; Score 1797; DB 2; Length 344;
Best Local Similarity 99.4%; Pred. No. 1.1e-140;
Matches 342; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy	1	MKTTPKWNHNSIAWIFTLGLAALCLFGQVPSRSGDAPFKAMDNVTVRQGSATLRCTID	60
Db	1	MKTTPKWNHNSMAWIFTLGLAALCLFGQVPSRSGDAPFKAMDNVTVRQGSATLRCTID	60
Qy	61	NRVTRVWLNRSTLYAGNDKWCCLDPRVLLSNTQTVSIEIQNVVDYDEGPTCSVQTD	120
Db	61	NRVTRVWLNRSTLYAGNDKWCCLDPRVLLSNTQTVSIEIQNVVDYDEGPTCSVQTD	120
Qy	121	NHPKTSRVHLIVQVSPKIVEISSDINIEGNNISLTCTIATGRPEPTVTRHISPKAVGV	180
Db	121	NHPKTSRVHLIVQVSPKIVEISSDINIEGNNISLTCTIATGRPEPTVTRHISPKAVGV	180


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RN RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Suganara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RL prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
[7]
RN RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuunai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaki S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RL sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
[8]
RN RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito K., Satoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toyota T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor (By
CC similarity).
CC
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CC -----
CC EMBL; AK045973; BAC32555.1; -; mRNA.
CC EMBL; AK046377; BAC32695.1; -; mRNA.
CC HSSP; P13596; 1Q21.
CC Ensembl; ENSMUSG0000059974; Mus musculus.
CC MGI; MGI:2446259; Hnt.
CC GO; GO:0016020; C:membrane; IEA.
CC GO; GO:0005515; F:protein binding; IEA.
CC GO; GO:0007155; P:cell adhesion; IEA.
CC InterPro; IPR013098; I-set.
CC InterPro; IPR003599; Ig.
CC InterPro; IPR007110; Ig-like.
CC InterPro; IPR003598; Ig.C2.
CC InterPro; IPR013151; Immunoglobulin.
CC SMART; SM00409; IG; 3.
CC SMART; SM00408; ICG2; 2.
CC PROSITE; PS00835; IG LIKE; 3.
KW Cell adhesion; Immunoglobulin domain; Membrane; Repeat.
SQ SEQUENCE 344 AA; 37941 MW; CDA5299D4CD86065 CRC64;
Query Match 98.6%; Score 1780; DB 2; Length 344;
Best Local Similarity 98.0%; Pred. No. 2.9e-139;
Matches 337; Conservative 5; Mismatches 2; Indels 0; Gaps 0;
QY 1 MKTIQPKHNSISWAIPTGLAALCLFQGVPRSGDATFPKAMDNVTVRQGESATLRCITID 60
DB 1 MKTIQAKHNSISWAIPTGLAALCLFQGVPRSGDATFPKAMDNVTVRQGESATLRCITID 60
QY 61 NRVTAVLNARSTILYAGNDKWCMLDPRVLLSNTQTQYSIEIQNVVDYDEGPTCYTCVOTD 120
DB 121 NHPKTSRVHLIVQSPKIVSEISSINISNEGNNISLTCTIATGRPPTVTRHISPKAVGFV 180
DB 121 NHPKTSRVHLIVQSPKIVSEISSINISNEGNNISLTCTIATGRPPTVTRHISPKAVGFV 180
QY 181 SEDEYLEIQITRQSGDGYECSASNDVAAPVVRVKVTVVPPYISBAKGTGVPVGQKGT 240
DB 181 SEDEYLEIQITRQSGEYECASNDVAAPVVRVKVTVVPPYISBAKGTGVPVGQKGT 240
QY 241 LQCEASVPSAEFQWYKDKRLIECKGKVKVKNRPFLSKLIFFNVSBDHYGNYTCVASNK 300
DB 241 LQCEASVPSAEFQWYKDKRLIECKGKVKVKNRPFLSKLIFFNVSBDHYGNYTCVASNK 300
QY 301 LGHTNASIMLFGPGCAVSEVNGTSRRACGCVLLPLLVHLHLKLF 344
DB 301 LGHTNASIMLFGPGCAVSEVNGTSRRACGCVLLPLLVHLHLKLF 344
RESULT 3
NTRI_HUMAN STANDARD; PRT: 344 AA.
AC Q9P121; Q6UKJ3; Q86VJ9;
DT 13-DEC-2002, integrated into UniProtKB/Swiss-Prot.
DT 01-OCT-2000, sequence version 1.
DT 07-MAR-2006, entry version 39.
DE Neurotrophin precursor (hnt).
GN Name=NT; ORFNames=UNQ297/PRO337;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM 1).
RA Li G., Jin J., Tan X., Hu S., Yuan J., Qiang B.;
RT "Cloning and identification of human neurotrophin full length cDNA.";
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
[2]
RN NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 2).
RX MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D.T., Brush J.,
RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA Eaton D., Foster J.S., Grimaldi C., Gu Q., Hass P.E., Heldens S.,
RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA Lewis L., Liao D., Mark M.R., Robbie E., Sanchez C., Schoenfeld J.,
RA Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
RA Vandlen R.L., Watanabe C., Wieand D., Woods K., Xie M.-H.,
RA Yansura D.G., Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A.D.,
RA Wood W.I., Godowski P.J., Gray A.M.;
RT "The secreted protein discovery initiative (SPDI), a large-scale
RT effort to identify novel human secreted and transmembrane proteins: a
RT bioinformatics assessment.";
RL Genome Res. 13:2265-2270(2003).
[3]
RN NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 3).
RC TISSUE=Skin;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Whiting J., Heiton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
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Query Match      91.2%; Score 1647.5; DB 1; Length 344;
Best Local Similarity 93.5%; Pred.No. 3e-128;
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QY 12 ISWAIFGLAALCLF---QGVPSRSGDATPPKAMDNVTVRQGESATLRCTIDNRTVRVAV 68
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      :
Db 9 LPWKCLVVVSLRLLLFLVPTGVPSRSGDATPPKAMDNVTVRQGESATLRCTIDNRTVRVAV 68

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Tammoja K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A., Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yagi K., Yamanihi H., Zabarovsky E., Zhu S., Zimmer A., Hide W., Bult C., Grimmond S.M., Teasdale R.D., Liu E.T., Brusic V., Ouackenbush J., Wahlstedt C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y., Fukuda S., Kanamaru-Katayama M., Suzuki M., Aoki J., Arakawa T., Lida J., Imamura K., Itoh M., Kato T., Kawaji H., Kawagashira N., Kawashima T., Kojima M., Kondo S., Konno H., Nakano K., Ninomiya N., Nishio T., Okada M., Plessey C., Shibata K., Shiraki T., Suzuki S., Tagami M., Waki K., Watahiki A., Okamura-Oho Y., Suzuki H., Kawai J., Hayashizaki Y.;
RT "The transcriptional landscape of the mammalian genome.";
RL Science 309:1559-1563(2005).
RN [3]
RP
RC STRAIN=C57BL/6J; TISSUE=Visual cortex;
RX PubMed=161414073; DOI=10.1126/science.1112009;
RG RIKEN Genome Exploration Research Group, and Genome Science Group
RG (Genome Network Core Team) and the FANTOM Consortium;
RT "Antisense Transcription in the Mammalian Transcriptome.";
RL Science 309:1564-1566(2005).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Visual cortex;
RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S., Nikaide I., Osato R., Saito K., Suzuki H., Yamanaka I., Kiyosawa H., Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T., Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J., Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W., Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S., Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S., Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J., Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D., Kanai A., Kawaji H., Kawagawa Y., Kedzierski R.M., King B.L., Kongaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A., Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H., Nagahima T., Nomura K., Okido T., Pavan W.J., Pextea G., Pesole G., Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S., Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M., Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K., Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M., Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C., Wilming L.G., Wyshaw-Boris A., Yanagisawa M., Yang I., Yang L., Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N., Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K., Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S., Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I., Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A., Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J., Birney E., Hayashizaki Y.;
RT "Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs";
RL Nature 420:563-573(2002).
RN [5]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Visual cortex;
RX MEDLINE=21036560; PubMed=11217851; DOI=10.1038/35055500;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Arakawa T., Hara A., Funahashi Y., Konno H., Adachi J., Fukuda S., Aizawa K., Izawa M., Nishikawa K., Kiyosawa H., Kondo S., Yamanaka I., Saïto T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saïto R., Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Fleischmann W., Gaasterland I., Gissi C., King B., Kochiya H., Kuhei P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., Schriml L.M., Staabli F., Suzuki R., Tomita M., Wagner L., Washio T., Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombere P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seva T., Shibata Y., Storch K.-F.,

Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohseki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RN Nature 409:685-690(2001).
[6]
RN
RC NUCLEOTIDE SEQUENCE.
RP STRAIN=C57BL/6J; TISSUE=Visual cortex;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
[7]
RN
RC NUCLEOTIDE SEQUENCE.
RP STRAIN=C57BL/6J; TISSUE=Visual cortex;
RX MEDLINE=20530913; PubMed=11078661; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoaka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishigine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watabiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawaji J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
[8]
RN
RC NUCLEOTIDE SEQUENCE.
RP STRAIN=C57BL/6J; TISSUE=Visual cortex;
RA Arakawa T., Carninci P., Fukuda S., Hashizume W., Hayashida K.,
RA Hori F., Iida J., Imamura K., Imotani K., Itoh M., Kanagawa S.,
RA Kawai J., Koijima M., Konno H., Murata M., Nakamura M., Ninomiya N.,
RA Nishiyori H., Nomura K., Ohno M., Sakazume N., Sano H., Sasaki D.,
RA Shibata K., Shiraki T., Tagami M., Takami Y., Waki K., Watanahi A.,
RA Muramatsu M., Hayashizaki Y.;
RT Submitted (MAR-2004) to the ENBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor (By
CC similarity).

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ENBL; AK158752; BAE3464.1; -; mRNA.
MGI; MGI:2446259; Hnt.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005155; F:protein binding; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPRO013098; I-set.
DR InterPro; IPRO03599; IG.
DR InterPro; IPRO07110; IG-like.
DR InterPro; IPRO03598; IG.c2.
DR InterPro; IPRO13151; Immunoglobulin.
DR SMART; SM00409; IG; 3.
DR SMART; SM00408; IGc2; 2.
DR PROSITE; PS50835; IG-LIKE; 3.
KW Cell adhesion; Immunoglobulin domain; Membrane; Repeat.

Query Match 90.9%; Score 1641.5; DB 2; Length 344;
Best Local Similarity 93.2%; Pred. No. 9.5e-128;
Matches 313; Conservative 8; Mismatches 12; Indels 3; Gaps

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Db : : :
9 LPWKCIWVSLRLFLVPFTGVPRSGDATFPKAMNDVTVRGGSATLRCTIDNRVTVAV
QY LNRSSTLYAGNDKCWLDPRVLLSNTQTQYSIEIQNVDDVDYDEGYTCSVTDNHPKTSRV
Db LNRSSTLYAGNDKCWLDPRVLLSNTQTQYSIEIQNVDDVDYDEGYTCSVTDNHPKTSRV
QY 129 HLIVQVSPIKEISSDINSINEGNISLTCIATGRPEPTVTRHSPXAVGFVSEDEYLEI

FT DISULFID 241 293 Potential.
FT VARSPLIC 310 320 Missing (in isoform 2).
FT /FTID=VSP 002607.
SQ SEQUENCE 353 AA; 38736 MW; 2550C48591EBBBA6 CRC64;

Query Match 81.8%; Score 1477.5; DB 1; Length 353;
Best Local Similarity 78.6%; Pred. No. 4.2e-114;
Matches 276; Conservative 32; Mismatches 32; Indels 11; Gaps 1;

QY 5 QPKMHSISWAIFTGLAALCLFQGVPRSGDATFPKAMDNVTVRQGESATLRCCTIDNRVT 64
DB 3 QAKMQHPVSWVIFAGMAALLLFQGVPRSGDATFPKAMDNVTVRQGESATLRCSDVNRVT 62
QY 65 RVAMLNRSSTILYAGNDKWCCLDRVLLSNTQYISIEIQNVVDVYDEGPPYTCVQTDNHPK 124
DB 63 RVAMLNRSSTILYAGNDKWCCLDRVLLSNTQYISIEIQNVVDVYDEGPPYTCVQTDNHPK 122
QY 125 TSVRLHIVQVSPKIVEISSDISINEGNNISLFCIATGRPEPTVTVRHHISPKAVGVSEDE 184
DB 123 TSVRLHIVQVSPKITESSDISINEGNNVSLTCIATGRPDPTITWRHISPKAVGFISEDE 182
QY 185 YLEIOGITREOSGDYECASNDVAAPVVRVVKVTVNYPPISEAKGTGVPVQKGTLOCE 244
DB 183 YLEITGITREOSGEYECASNDVAAPVVRVVKVTVNYPPIYSDAKSTGVPVQKGTLMCE 242
QY 245 ASAVPSAEFQWKDDKRLIEGKGVKVENRPLSKLIFPNVSEHDYGNVTCVASKNGLHT 304
DB 243 ASAVPSADFQWKDDKRLAEGQKGLKVENKAPFSLTFFNVSEQDYGNVTCVASKNGLNT 302
QY 305 NASIMLF-----GPGAVSEVSGTSTRAGCVMLPLLLVLLHLKLF 344
DB 303 NASMILYEITTTALTPWKGPAGVHDGNSGAWRGSCAWLLALPLAQLARQF 353

RESULT 9
ID O57596 CHICK PRELIMINARY; PRT; 313 AA.
AC O57596
DT 01-JUN-1998, integrated into UniProtKB/TrEMBL.
DT 01-JUN-1998, sequence version 1.
DT 07-FEB-2006, entry version 31.
DE Neural secreted glycoprotein (CEPU-Se alpha 2 isoform).
GN Name=CEPU; Synonyms=CEPU-Se;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=99347334; PubMed=10420985;
RA Kim D.S., Rhew T.H., Moss D.J., Kim J.Y.;
RT "cDNA cloning of the CEPU, a secreted type of neural glycoprotein
RT belonging to the immunoglobulin-like opioid binding cell adhesion
RT molecule (OBCAM) subfamily";
RL Mol. Cells 9:270-276 (1999).
RN [2]
RN NUCLEOTIDE SEQUENCE.
RA Kim D.;
RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Brain;
RA Lodge A.P., McNamee C.J., Howard M.R., Reed J.E., Moss D.J.;
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor (By
CC similarity).
CC
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC
CC EMBL; AJ225897; CAA12649.1; -; Genomic_DNA.
DR EMBL; AF292935; AAG01878.1; -; mRNA.

DR HSSP; Q9UQH9; IDUS.
DR Ensembl; ENSGALG00000001437; Gallus gallus.
DR GO; GO:0005515; P:protein binding; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR013098; I-set.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG C2.
DR InterPro; IPR013151; Immunoglobulin.
DR SMART; SM00409; IG; 3.
DR SMART; SM00408; IGC2; 2.
DR PROSITE; PS00835; IG LIKE; 3.
KW Cell adhesion; Immunoglobulin domain; Membrane; Repeat.
SQ SEQUENCE 313 AA; 34482 MW; 99AD825CAE4A5347 CRC64;

Query Match 79.1%; Score 1428; DB 2; Length 313;
Best Local Similarity 85.4%; Pred. No. 4.6e-110;
Matches 263; Conservative 27; Mismatches 18; Indels 0; Gaps 0;

QY 5 QPKMHSISWAIFTGLAALCLFQGVPRSGDATFPKAMDNVTVRQGESATLRCCTIDNRVT 64
DB 3 QAKMQHPVSWVIFAGMAALLLFQGVPRSGDATFPKAMDNVTVRQGESATLRCSDVNRVT 62
QY 65 RVAMLNRSSTILYAGNDKWCCLDRVLLSNTQYISIEIQNVVDVYDEGPPYTCVQTDNHPK 124
DB 63 RVAMLNRSSTILYAGNDKWCCLDRVLLSNTQYISIEIQNVVDVYDEGPPYTCVQTDNHPK 122
QY 125 TSVRLHIVQVSPKIVEISSDISINEGNNISLTCIATGRPEPTVTVRHHISPKAVGVSEDE 184
DB 123 TSVRLHIVQVSPKITESSDISINEGNNVSLTCIATGRPDPTITWRHISPKAVGFISEDE 182
QY 185 YLEIOGITREOSGDYECASNDVAAPVVRVVKVTVNYPPISEAKGTGVPVQKGTLOCE 244
DB 183 YLEITGITREOSGEYECASNDVAAPVVRVVKVTVNYPPIYSDAKSTGVPVQKGTLMCE 242
QY 245 ASAVPSAEFQWKDDKRLIEGKGVKVENRPLSKLIFPNVSEHDYGNVTCVASKNGLHT 304
DB 243 ASAVPSADFQWKDDKRLAEGQKGLKVENKAPFSLTFFNVSEQDYGNVTCVASKNGLNT 302
QY 305 NASIMLF 312
DB 303 NASMILYG 310

RESULT 10
ID O93242 CHICK PRELIMINARY; PRT; 344 AA.
AC O93242;
DT 01-NOV-1998, integrated into UniProtKB/TrEMBL.
DT 01-NOV-1998, sequence version 1.
DT 07-FEB-2006, entry version 29.
DE CEPU-1.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Kimura Y., Shirabe K., Fukushima M., Takeshita M., Tanaka H.;
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor (By
CC similarity).
CC
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC
CC EMBL; AB011810; BAA31514.1; -; mRNA.
DR HSSP; Q9UQH9; IDUS.
DR Ensembl; ENSGALG00000001437; Gallus gallus.
DR GO; GO:0005515; P:protein binding; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR013098; I-set.

```

DR InterPro: IPR003599; Ig.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003598; Ig_c2.
DR InterPro: IPR013151; Immunoglobulin.
DR SMART: SM00409; IG; 3.
DR SMART: SM00408; IGC2; 2.
DR PROSITE: PS00835; IG_LIKE; 3.
KW Cell adhesion; Immunoglobulin domain; Membrane; Repeat.
SQ SEQUENCE 344 AA; 37614 MW; 25CAABF526A6B57E CRC64;

Query Match 79.0%; Score 1427.5; DB 2; Length 344;
Best Local Similarity 79.2%; Pred. No. 5.8e-110;
Matches 267; Conservative 31; Mismatches 36; Indels 3; Gaps 1;

QY 11 SISWAIFGLAALCLF---QGVPRSGDATFPKAMDNVTVRQGESATLRCTIDNRVTRVA 67
DB 8 ALPWRCLVLCRLFLVPAGVPVRSGDATFPKAMDNVTVRQGESATLRCSVDNRVTRVA 67
QY 68 WLNRSITLYAGNDKWCCLDPRVLLSNTQYISIEIONVDVYDEGPTCSVQTDNHPKTSR 127
DB 68 WLNRSITLYAGNDKWCCLDPRVLLSNTQYISIEIONVDVYDEGPTCSVQTDNHPKTSR 127
QY 128 VHLIVQVSPKIVEISSDISINEGNNISLTCTIATGRPEPTVTRHISPKAVGFSEDEYLE 187
DB 128 VHLIVQVSPKITEISSDISINEGNNISLTCTIATGRPDPTITWRHISPKAVGFSEDEYLE 187
QY 188 IQGITREQSGDYECASNDVAAPVVRVKVTNYPPISEAKGTGVPVGQKGLTQCEASA 247
DB 188 ITGITREQSGDYECASNDVAAPVVRVKVTNYPPISEAKGTGVPVGQKGLTQCEASA 247
QY 248 VPSAEFQWKDKRLIEGKGVKVENRPFSLKLIFFNVSEHDYGYNTCVASNKLGHNTAS 307
DB 248 VPSADFQWKDKRLIEGKGVKVENRPFSLKLIFFNVSEHDYGYNTCVASNKLGHNTAS 307
QY 308 IMLFG 312
DB 308 MILYFG 312

RESULT 12
Q6DFY2_MOUSE PRELIMINARY; PRT; 337 AA.
AC Q6DFY2;
DT 16-AUG-2004, integrated into UniProtKB/TrEMBL.
DT 21-FEB-2006, entry version 1.
DE Opioid binding protein/cell adhesion molecule-like.
GN Names: Opioid;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6; TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heich F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";

DR InterPro: IPR003599; Ig.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003598; Ig_c2.
DR InterPro: IPR013151; Immunoglobulin.
DR SMART: SM00409; IG; 3.
DR SMART: SM00408; IGC2; 2.
DR PROSITE: PS00835; IG_LIKE; 3.
KW Cell adhesion; Immunoglobulin domain; Membrane; Repeat.
SQ SEQUENCE 344 AA; 37614 MW; 25CAABF526A6B57E CRC64;

Query Match 79.0%; Score 1427.5; DB 2; Length 344;
Best Local Similarity 79.2%; Pred. No. 5.8e-110;
Matches 267; Conservative 31; Mismatches 36; Indels 3; Gaps 1;

QY 11 SISWAIFGLAALCLF---QGVPRSGDATFPKAMDNVTVRQGESATLRCTIDNRVTRVA 67
DB 8 ALPWRCLVLCRLFLVPAGVPVRSGDATFPKAMDNVTVRQGESATLRCSVDNRVTRVA 67
QY 68 WLNRSITLYAGNDKWCCLDPRVLLSNTQYISIEIONVDVYDEGPTCSVQTDNHPKTSR 127
DB 68 WLNRSITLYAGNDKWCCLDPRVLLSNTQYISIEIONVDVYDEGPTCSVQTDNHPKTSR 127
QY 128 VHLIVQVSPKIVEISSDISINEGNNISLTCTIATGRPEPTVTRHISPKAVGFSEDEYLE 187
DB 128 VHLIVQVSPKITEISSDISINEGNNISLTCTIATGRPDPTITWRHISPKAVGFSEDEYLE 187
QY 188 IQGITREQSGDYECASNDVAAPVVRVKVTNYPPISEAKGTGVPVGQKGLTQCEASA 247
DB 188 ITGITREQSGDYECASNDVAAPVVRVKVTNYPPISEAKGTGVPVGQKGLTQCEASA 247
QY 248 VPSAEFQWKDKRLIEGKGVKVENRPFSLKLIFFNVSEHDYGYNTCVASNKLGHNTAS 307
DB 248 VPSADFQWKDKRLIEGKGVKVENRPFSLKLIFFNVSEHDYGYNTCVASNKLGHNTAS 307
QY 308 IMLFG 312
DB 308 MILYFG 312

RESULT 11
Q9DGI5_CHICK PRELIMINARY; PRT; 315 AA.
AC Q9DGI5;
DT 01-MAR-2001, integrated into UniProtKB/TrEMBL.
DT 07-FEB-2006, entry version 1.
DE CEPU-Se alpha 1 isoform.
GN Name=CEPU-Se;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Brain;
RA Lodge A.P., McNamee C.J., Howard M.R., Reed J.E., Moss D.J.;
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor
CC similarity).
CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
CC EMBL; AF292936; AAG01879.1; -, mRNA.
CC HSP; Q9UQH9; 1DJS.
CC Ensembl; ENSGALG0000001437; Gallus gallus.
CC GO; GO:0005515; P:protein binding; IEA.
CC GO; GO:0007155; P:cell adhesion; IEA.
CC InterPro; IPR013098; I-set.
CC InterPro; IPR003599; IG.
CC InterPro; IPR007110; Ig-like.
CC InterPro; IPR003598; Ig_c2.

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RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=CS7BL/6; TISSUE=Brain;
RA Director MGC Project;
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
CC -----
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CC -----
DR EMBL; BC076581; AAH76581.1; -; mRNA.
DR IntAct; Q6DFY2; -.
DR Ensembl; ENSMUSG0000062257; Mus musculus.
DR MGI; MGI:97397; Opcml.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig C2.
DR InterPro; IPR013151; Immunoglobulin.
DR InterPro; IPR013106; V-set.
DR SMART; SM00409; IG; 3.
DR SMART; SM00408; IGC2; 2.
DR PROSITE; PS50835; IG LIKE; 3.
KW Immunoglobulin domain; Membrane; Transmembrane.
SQ SEQUENCE 337 AA; 37156 MW; 2A279D982E60F4B CRC64;

Query Match 72.3%; Score 1306; DB 2; Length 337;
Best Local Similarity 72.1%; Pred. No. 7.1e-100;
Matches 243; Conservative 35; Mismatches 59; Indels 0; Gaps 0;

QY 8 MHNISWAIFTGLAALCLFQGVPSGDTATPKAMDNVTVRQGESATLRCTIDNRVTRVA 67
DB 1 MYHPAYWIVFSTATTALLFTFGVPVSGDTATPKAMDNVTVRQGESATLRCTIDNRVTRVA 60

QY 68 WLNRTSLIYAGNKKVCLDPRVLLSNTQVTSIEIQNVVDVDEGPTCSVQTDNHPKTSR 127
DB 61 WLNRTSLIYAGNKKVCLDPRVLLSNTQVTSIEIQNVVDVDEGPTCSVQTDNHPKTSR 120

QY 128 VHLIVQVSPKIVEISSDISINEGNNISLTCTATGRPEPTVTRHLSPKAVGFVSEDEYLE 187
DB 121 VHLIVQVPPQIVNMISSDITVNEGSSVTLMLCLAFGRPEPTVTRHLSGKGQGVSEDEYLE 180

QY 188 IQGIVREOSGDYECASNDVAAPVRRVKVTNYPPIYSEAKGTGVPVQKGTLCQESA 247
DB 181 ISDIKRDOSGEVCSALNDVAAPVRRVKVTNYPPIYSEAKGTGVPVQKGTLCQESA 240

QY 248 VPSAEFQWKDKRLIEGKGVKVENRPPPLSKLIEFNVSSEHDYGNVTCVASKLGHNTAS 307
DB 241 VPMASFQWPKEDTRLATGLDGVRIENKGRISTLTFFNVSEKDYGNVTCVATNKLGNWAS 300

QY 308 IMLFGPGAVSEVNSGTSRRAGCWLLPLLVLHLLKPF 344
DB 301 ITLYPGGAVIDGVNSASRALACLWLSGTFFAHFFIKF 337

RESULT 13
OBCAM_CHICK
ID OBCAM_CHICK STANDARD; PRT; 337 AA.
AC Q98892;
DT 01-NOV-1997, integrated into UniProtKB/Swiss-Prot.
DT 30-MAY-2000, sequence version 2.
DT 07-MAR-2006, entry version 43.
DE Opioid-binding protein/cell adhesion molecule homolog precursor
DE (Neurite inhibitor GP55-A) (OBCAM protein gamma isoform).
GN Name=OBCML;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA].
RC TISSUE=Brain;

```

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RA Lodge A.P., Kim D.-S., Howard M.R., McNamee C.J., Smith N., Moss D.J.;
RT "Cloning of CEPU-s, a secreted isoform of CEPU-1, and OBCAM cDNAs from
FT chick; structural diversity of IGLON family proteins.";
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE [MRNA] OF 64-337, AND PARTIAL PROTEIN SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=97157768; PubMed=9004047;
RA Wilson D.J.A., Kim D.-S., Clarke G.A., Marshall-Clarke S., Moss D.J.;
RT "A family of glycoproteins (GP55), which inhibit neurite outgrowth,
FT are members of the Ig superfamily and are related to OBCAM,
RL neurotrimin, LAMP and CEPU-1.";
RN J. Cell Sci. 109:3129-3138 (1996).
CC -!- FUNCTION: Inhibits neurite outgrowth.
CC -!- SUBCELLULAR LOCATION: Cell membrane; lipid-anchor; GPI-anchor.
CC -!- TISSUE SPECIFICITY: Restricted to the nervous system.
CC -!- DEVELOPMENTAL STAGE: Increases during development from very low
CC levels at embryonic day 10 and is most abundant after hatching.
CC -!- SIMILARITY: Belongs to the immunoglobulin superfamily. IGLON
CC family.
CC -!- SIMILARITY: Contains 3 Ig-like C2-type (immunoglobulin-like)
CC domains.
CC -----
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CC -----
DR EMBL; Y08170; CAB41420.1; -; mRNA.
DR HSPF; P78310; IFSW.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig C2.
DR InterPro; IPR013151; Immunoglobulin.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00409; IG; 3.
DR SMART; SM00408; IGC2; 2.
DR PROSITE; PS50835; IG LIKE; 3.
KW Cell adhesion; Direct protein sequencing; Glycoprotein; GPI-anchor;
KW Immunoglobulin domain; Lipoprotein; Membrane; Repeat; Signal.
FT SIGNAL 1 20 By similarity.
FT CHAIN 21 314 Opioid-binding protein/cell adhesion
FT molecule homolog.
FT /FTID=PRO.0000015063.
FT /FTID=PRO.0000015064.
FT PROPEP 315 337 Removed in mature form (Potential).
FT DOMAIN 32 119 Ig-like C2-type 1.
FT DOMAIN 129 211 Ig-like C2-type 2.
FT DOMAIN 215 302 Ig-like C2-type 3.
FT LIPID 314 314 GPI-anchor amidated asparagine
FT (Potential).
FT CARBOHYD 133 133 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 277 277 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 285 285 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 298 298 N-linked (GlcNAc...) (Potential).
FT DISULFID 50 108 Potential.
FT DISULFID 150 194 Potential.
FT DISULFID 236 288 Potential.
SQ SEQUENCE 337 AA; 36887 MW; BAE717551856651E CRC64;

Query Match 72.3%; Score 1305; DB 1; Length 337;
Best Local Similarity 73.2%; Pred. No. 8.6e-100;
Matches 248; Conservative 34; Mismatches 53; Indels 4; Gaps 2;

QY 8 MHNISWAIFTGLAALCLFQGVPSGDTATPKAMDNVTVRQGESATLRCTIDNRVTRVA 67
DB 1 MYHPACWIVFTATTALLFTFGVPVSGDTATPKAMDNVTVRQGESATLRCTIDNRVTRVA 60

QY 68 WLNRTSLIYAGNKKVCLDPRVLLSNTQVTSIEIQNVVDVDEGPTCSVQTDNHPKTSR 127
DB 61 WLNRTSLIYAGNKKVCLDPRVLLSNTQVTSIEIQNVVDVDEGPTCSVQTDNHPKTSR 120

QY 128 VHLIVQVSPKIVEISSDISINEGNNISLTCTATGRPEPTVTRHLSPKAVGFVSEDEYLE 187
DB 121 VHLIVQVPPQIVNMISSDITVNEGSSVTLMLCLAFGRPEPTVTRHLSGKGQGVSEDEYLE 180

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Qy 188 IQGTRQSGDYECASNDVAAPVVRVKVTVNYPYVISEAKGTGVPGKGTLOCEASA 247
 Db 181 ITGTRQSGDYECASNDVAAPVVRVKVTVNYPYVISEAKGTGVPGKGTLOCEASA 240
 Qy 248 VPSAEFQWYKDKRLIEGKGVKVENPFLSKLFFNVSEHDYGNVYCVASNKLGHNTAS 307
 Db 241 VPVAFQWFKEDTRLANGLEVRIESKRLSTLTFNVSEKDYGNVYCVATNKLGNNTAS 300
 Qy 308 IMFPGCAVSEVSGTERRAG--CWLLPLVLVHLHLKF 344
 Db 301 IILYPGCAVHDSGNAASRAAGLCLW--ATLLARLLDLDF 337

RESULT 14
 Q3TYL3 MOUSE
 ID Q3TYL3 MOUSE PRELIMINARY; PRT; 337 AA.
 AC Q3TYL3
 DT 11-OCT-2005, integrated into UniProtKB/TrEMBL.
 DT 11-OCT-2005, sequence version 1.
 DT 07-MAR-2006, entry version 9.
 DE Visual cortex cDNA, RIKEN full-length enriched library,
 DE clone:K230009E18 product:Opioid binding protein/cell adhesion molecule
 DE (OBAM) (Opioid-binding cell adhesion molecule) (OPCML) homolog.
 GN Name=Opcln;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Muridae; Murinae; Mus.
 OC NCBI_TaxId=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Visual cortex;
 RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
 RA Carninci P., Hayashizaki Y.;
 RT "High-efficiency full-length cDNA cloning.";
 RL Methods Enzymol. 303:19-44 (1999).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Visual cortex;
 RX PubMed=16141072; DOI=10.1126/science.1112014;
 RA Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,
 RA Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,
 RA Bajic V.B., Bremner S.E., Batalov S., Forrest A.R., Allen J.E.,
 RA Davis M.J., Wilming L.G., Aidinis V., Allen J.E.,
 RA Bansal M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M.,
 RA Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R.,
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 RC STRAIN=C57BL/6J; TISSUE=Visual cortex;
 RX PubMed=16141073; DOI=10.1126/science.1112009;
 RG RIKEN Genome Exploration Research Group, and Genome Science Group
 RG (Genome Network Core Team) and the FANTOM Consortium;
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 RC STRAIN=C57BL/6J; TISSUE=Visual cortex;
 RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
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 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Visual cortex;
 RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
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RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
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RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
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RC STRAIN=C57BL/6J; TISSUE=Visual cortex;
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RA Hori F., Iida J., Inamura K., Imotani K., Itoh M., Kanagawa S.,
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RA Muramatsu M., Hayashizaki Y.;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
CC CC
CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor (By similarity).
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CC
CC
CC EMBL; AK158538; BAE34550.1; -; mRNA.
CC MGI; MGI:97397; Opcml.
CC GO; GO:0016021; C:integral to membrane; IEA.
CC InterPro; IPR003599; IG.
CC InterPro; IPR007110; IG-like.
CC InterPro; IPR003598; IG c2.
CC InterPro; IPR013151; Immunoglobulin.
CC InterPro; IPR013106; V-set.
CC Pfam; PF00047; IG 2.
CC Pfam; PF07686; V-set; 1.
CC SMART; SM00409; IG; 3.
CC SMART; SM00408; IGC2; 2.
CC PROSITE; PS50835; IG-LIKE; 3.
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Db 181 ISDIKRDQSGEYECASNDVAAPDVRVKVITVNPPIYSKAKNTGVSVGKGLSCEASA 240
Qy 247 AVPSAEFQWKDKRLIEGKGVKVENRPFSLKLIFFNVSEHDYGNVTCVASNKLGHNTNA 306

Qy 248 VPSAEFQWKDKRLIEGKGVKVENRPFSLKLIFFNVSEHDYGNVTCVASNKLGHNTNA 307
Db 241 VPMAEFQWFKEDTFLATGLDGVRIENKGRISTLTFNVSEKDYGNVTCVATNKLGNINA 300
Qy 308 IMLPFGAVSEVNGTSRRRAGCVWLLPLLVHLLKLF 344
Db 301 ITLYEPGAVIDGVNSASRALACLWLSGTFFAHFFIKF 337
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AC Q723W6;
DT 01-OCT-2003, integrated into UniProtKB/TrEMBL.
DT 01-OCT-2003, sequence version 1.
DT 21-FEB-2006, entry version 23.
DE Hypothetical protein DKF2P686H1949.
GN Name=DKF2P686H1949;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
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RN [1]
RC NUCLEOTIDE SEQUENCE.
RC TISSUE=Human amygdala;
RA Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,
RA Fobo G., Han M., Wilemann S.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
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CC
CC
CC EMBL; BX337377; CAD97619.1; -; mRNA.
CC HSSP; Q9UQH9; ILIL.
CC Ensembl; ENSG00000183715; Homo sapiens.
CC GO; GO:0005515; F:protein binding; IEA.
CC GO; GO:0004872; F:receptor activity; IEA.
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Best Local Similarity 71.6%; Pred. No. 5.3e-99;
Matches 242; Conservative 38; Mismatches 57; Indels 1; Gaps 1;
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Qy 247 AVPSAEFQWKDKRLIEGKGVKVENRPFSLKLIFFNVSEHDYGNVTCVASNKLGHNTNA 306

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